

## **FIGURE 1**

ACTGCACCTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTCGACCTCGA  
CCCACCGCGTCCGGGCCGGAGCAGCACGGCCGCAGGACCTGGAGCTCCGGCTGCGTCTTCCCG  
CAGCGCTACCCGCCATGCGCTGCCGCCGGCCGCGCTGGGGCTCCTGCCGCTTCTGCTG  
CTGCTGCCGCCGCCGGAGGCCAAGAAGCCGACGCCCTGCCACCGGTGCCGGGGCT  
GGTGGACAAGTTAACCAAGGGATGGTGGACACCGCAAAGAAGAACCTTGGCGGGAAACA  
CGGCTTGGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTGCCCTGCTGGAGATC  
CTGGAGGGCTGTGCAGAGCAGCGACTTCGAATGCAATCAGATGCTAGAGGCGCAGGAGGA  
GCACCTGGAGGCCTGGTGGCTGCAGCTGAAGAGCGAATATCCTGACTTATTGAGTGGTTT  
GTGTGAAGACACTGAAAGTGTGCTGCTCTCCAGGAACCTACGGTCCCACTGTCTCGCATGC  
CAGGGCGGATCCCAGAGGCCCTGCAGCGGAATGCCACTGCAGCGAGATGGAGCAGACA  
GGGCGACGGGTCTGCCGGTGCACATGGGTACCAGGGCCGCTGTGCACTGACTGCATGG  
ACGGCTACTTCAGCTCGCTCCGAACGAGACCCACAGCATCTGCACAGCCTGTGACGAGTCC  
TGCAAGACGTGCTCGGCCTGACCAACAGAGACTGCGCGAGTGTGAAGTGGCTGGGTGCT  
GGACGAGGGCGCCTGTGGATGTGGACGAGTGTGCAGGCCGAGCCGCTCCCTGCAGCGCTG  
CGCAGTTCTGTAAGAACGCCAACGGCTCCTACACGTGCGAAGAGTGTGACTCCAGCTGTG  
GGCTGCACAGGGGAAGGCCAGGAAACTGTAAAGAGTGTATCTCTGGCTACGCGAGGGAGCA  
CGGACAGTGTGCAGATGTGGACGAGTGTCACTAGCAGAAAAACCTGTGTGAGGAAAAACG  
AAAATGCTACAATACTCCAGGGAGCTACGTCTGTGTGTGCCTGACGGCTTCGAAGAACG  
GAAGATGCCTGTGTGCCGCCAGAGGGCTGAAGCCACAGAAGGAGAAAGCCGACACAGCT  
GCCCTCCCGGAAGACCTGTAATTGTGCCGGACTTACCCCTAAATTATTACAGAAGGATGTCC  
CGTGGAAAATGTGGCCCTGAGGATGCCGTCTCCTGCAGTGGACAGCGGGGGAGAGGCTGC  
CTGCTCTCTAACGGTGATTCTCATTGTCCCTAAACAGCTGCATTCTGGTTGTTCTTA  
AACAGACTTGTATATTTGATACAGTTCTTGTAAATAAAATTGACCATTGTAGGTAATCAGG  
AGGAAAAAAAGGGCGCCGCGACTCTAGAGTCGACCTGCAGAAGC  
TTGGCCGCCATGGCCAACTTGTTTATTGCAGCTTATAATGGTACAAATAAGCAATAGCA  
TCACAAATTCAAAATAAGCATTTCAGCATTCTAGTTGTGGTTGTCCAAACTC  
ATCAATGTATCTTATCATGTCTGGATCGGGATTAAATTCCGGCGCAGCACCATGGCCTGAAAT  
AACCTCTGAAAGAGGAACTTGGTTAGGTACCTCTGAGGCGAAAGAACCGACTGTGGAATG  
TGTGTCAGTTAGGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAGCATGC  
ATCTCAATTAGTCAGCAACCCAGTTT

## FIGURE 2

><subunit 1 of 1, 353 aa, 0 stop

><MW: 38192, pI: 4.53, NX(S/T): 2

MRLPRAALGLPLLLLPPAPEAAKKPTPCHRCGLVDKFNQGMVDTAKKNFGGGNTAEEKTLSKYESSEIRL  
LEILEGLCESSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFCVKVCCSPGTYGPDCLACQGGSQRPCSG  
NGHCGSGDGRQGDGSCRCHMGYQGPLCTDCMDGYFSSLRNETHSICTACDESCKTCGTLNRDCGECEVGWVLDE  
GACVDVDECAAEP PCSAAQFCKNANGSYTCEECDSSCVGCTGEGPGNC E C I S G Y A R E H G Q C A D V D E C S L A E K T  
CVRKNENCYNTPGSYVCVCPDGFEETEDACVPPAEEATEGESPTQLPSREDL

**Signal peptide:**

amino acids 1-24

**N-glycosylation sites.**

amino acids 190-194 and 251-255

**Glycosaminoglycan attachment sites.**

amino acids 149-153 and 155-159

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 26-30

**Casein kinase II phosphorylation sites.**

amino acids 58-62, 66-70, 86-90, 197-201, 210-214, 255-259, 295-299, 339-343  
and 349-353

**Tyrosine kinase phosphorylation site.**

amino acids 303-310

**N-myristoylation sites.**

amino acids 44-50, 54-60, 55-61, 81-87, 150-156, 158-164, 164-170, 252-258 and  
313-319

**Aspartic acid and asparagine hydroxylation site.**

amino acids 308-320

**EGF-like domain cysteine pattern signature.**

amino acids 166-178

**Leucine zipper pattern.**

amino acids 94-116

## FIGURE 3

CAGGTCCAAC TGCACCTCGTTCTATCGATTGAATTCCCCGGGATCCTCTAGAGATCCCTC  
GACCTCGACCCACGCGTCCGCCAGGCCGGAGGCAGCGCCCAGCGTCTAACGGGAACA  
GCCCTGGCTGAGGGAGCTGCAGCGCAGCAGAGTATCTGACGGCCAGGTTGCGTAGGTGCG  
GCACGAGGAGTTTCCCGCAGCGAGGAGGTCTGAGCAGCATGGCCCAGGAGCGCCTTC  
CCTGCCGCCGCTCTGGCTCTGGAGCATCCTCCTGTGCCTGCGACTGCAGGGCGGAGGC  
CGGGCCGCCAGGAGGAGGCCTGTACCTATGGATCGATGCTCACCAAGGCAAGAGTACTCA  
TAGGATTGAAGAAGATATCCTGATTGTTAGAGGGAAAATGGCACCTTTACACATGAT  
TTCAGAAAAGCGAACAGAGAATGCCAGCTATTCTGTCAATATCCATTCCATGAATTTCAC  
CTGGCAAGCTGCAGGGCAGGCAGAATACTTCTATGAATTCTGTCCCTGCGCTCCCTGGATA  
AAGGCATCATGGCAGATCCAACCGTCAATGTCCCTGTGGAAACAGTGCCTCACAGGCA  
TCAGTTGTTCAAGTTGGTTCCATGTCTGGAAAACAGGATGGGTGGCAGCATTGAAAGT  
GGATGTGATTGTTATGAATTCTGAAGGCAACACCATTCTCAAACACCTCAAAATGCTATCT  
TCTTAAACATGTCAACAAGCTGAGTGCCTGATGGGTTCCACGGACCTCACTGTGAGAAAGCC  
TACCCACGATGTATGAATGGTGGACTTGTGACTCCTGGTTCTGCATCTGCCACCTG  
GATTCTATGGAGTGAACGTGACAAAGCAAACGCTCAACCACCTGCTTAATGGAGGGACC  
TGTTCTACCCCTGGAAAATGTATTGCCCTCAGGACTAGAGGGAGAGCAGTGTGAAATCAG  
CAAATGCCACAACCCTGTGAAATGGAGGTAAATGCATTGGTAAAAGCAAATGTAAGTGT  
CCAAAGGTTACCAGGGAGACCTCTGTTCAAAGCCTGTCTGCAGCCTGGCTGTGGC  
GGAACCTGCCATGAACCCAAACAAATGCCAATGTCAAGAAGGTTGGCATGGAAGACACTGCAA  
TAAAGGTACGAAGCCAGCCTCATACATGCCCTGAGGCCAGCAGCGCCAGCTCAGGCAGC  
ACACGCCCTCACTTAAAAGGCCAGGGAGCGGGGATCCACCTGAATCCAATTACATCTGG  
TGAACTCCGACATCTGAAACGTTTAAGTTACACCAAGTTACAGCCTTGTAAACCTTCA  
TGTGTTGAATGTTCAAATAATGTTCATTACACTTAAGAATACTGGCCTGAATTATTAGCT  
TCATTATAAATCACTGAGCTGATATTACTCTCCTTTAAGTTCTAAGTACGTCTGTAG  
CATGATGGTATAGATTCTTGTTCAGTGCCTGGACAGATTATATTATGTCAATTGA  
TCAGGTTAAAATTTCAGTGTAGTTGGCAGATATTCTAAACATTACAATGCATTATGGT  
GTCTGGGGCAGGGAAACATCAGAAAGGTTAAATTGGGAAAATGCGTAAGTCACAAGAAT  
TTGGATGGTGCAGTTAATGTTGAAGTTACAGCATTTCAGATTATTGTAGATATTAGAT  
GTTTGTACATTAAAATTGCTCTAATTAACTCTCAATACAATATATTGACC  
TTACCATTATTCCAGAGATTCACTATTAAAAAAATTACACTGTGGTAGTGGCATT  
AAACAATATAATATTCTAAACACAATGAAATAGGGAAATATAATGTATGAACCTTTGCAT  
TGGCTTGAAGCAATAATATATTGTAACAAAACACAGCTCTACCTAATAACATT  
ACTGTTGTATGTATAAAATAAGGTGCTGCTTAGTTTTGGAAAAA  
AAAAAAAAAAAAAAAAAAGGCCGGCGCAGCTAGAGTCGACCTGCAGAAGCTTGGC  
CGCCATGGCCCAACTGTTATTGCAGCTTATAATG

## **FIGURE 4**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33094
><subunit 1 of 1, 379 aa, 0 stop
><MW: 41528, pI: 7.97, NX(S/T): 2
MARRSAFPAAALWLWSILLCLLALRAEAGPPQEESLYLWIDAHQARVLIGFEEDILIVSEGK
MAPFTHDFRKAQQRMPAIPVNIHSMNFTWQAAGQAEYFYEFLSLRSLDKGIMADPTVNVPPLL
GTVPHKASVVQVGFPCLGKQDGVAAFEVDVIVMNSEGNTILQTPQNAIFFKTCQQAECPGGC
RNGGFCNERRICECPDGFHGPCEKALCTPRCMNGGLCVTPGFCICPPGFYGVNCDKANCST
TCFNGGTCFYPGKCI CPPGLEGEQCEISKCPQPCRNGGKCI GSKSKCKCSKGYQGDLCSPKVC
EPGCGAHGTCHEPNKCQCQEGWHGRHCNKRYEASLIHALRPAGAQLRQHTPSLKKAEERRDP
PESNYIW
```

**Signal peptide:**

amino acids 1-28

**N-glycosylation site.**

amino acids 88-92, 245-249

**Casein kinase II phosphorylation site.**

amino acids 319-323

**Tyrosine kinase phosphorylation site.**

amino acids 370-378

**N-myristoylation sites.**

amino acids 184-190, 185-191, 189-195, 315-321

**ATP/GTP-binding site motif A (P-loop).**

amino acids 285-293

**EGF-like domain cysteine pattern signature.**

amino acids 198-210, 230-242, 262-274, 294-306, 326-338

## **FIGURE 5**

CGGACGGCGGGCGTCCGGCGTCGAGAGCCAGGAGGCCAGGAGGCCAGGAGGCCACCATGTGGCGATGTCCACTGGGGCTAC  
TGCTGTTGCTGCCGCTGGCTGGCCACTTGGCTCTGGCTCGGGCAGCAGGGCTGTGGCGCCGG  
GAGCTAGCACCGGGCTGCACCTGCAGGGCATCCGGACGCCAGGGAGGCCGGTACTGCCAGGA  
GCAGGACCTGTGCTGCCGCGGCCGTGCCGACGACTGTGCCCTGCCACTCGGGGCCATCT  
GTTACTGTGACCTCTCTGCAACCGCACGGCTCCGACTGCTGCCCTGACTCTGGGACTTC  
TGCCTCGGCGTGCCACCCCTTTCCCCGATCCAAGGATGTATGCATGGAGGTGCTATCTA  
TCCAGTCTTGGAACGTACTGGACAACGTGAACCGTTCACCTGCCAGGAGAACAGGCAGT  
GGCATGGTGGATCCAGACATGATCAAAGCCATCAACCAGGGCAACTATGGCTGGCAGGCTGG  
GAACCACAGCGCCTCTGGGGCATGCCCTGGATGAGGGCATTGCTACGCCCTGGGACCA  
TCCGCCATCTCCTCGGTATGAAACATGCAATGAAATTATACAGTGCTGAACCCAGGGAG  
GTGCTTCCCACAGCCTCGAGGCCTCTGAGAAAGTGGCCAACCTGATTGATGAGCCTTGA  
CCAAGGCAACTGTGCAAGGCTCTGGGCTTCTCCACAGCAGCTGTCATCCGATCGTGTCT  
CAATCCATTCTCTGGGACACATGACGCCCTGTCCGTGCCCCAGAACCTGCTGTGAC  
ACCCACCAGCAGCAGGGCTGCCGCGGTGGCGTCTCGATGGTGCCTGGTGGTTCTGCGTCG  
CCGAGGGGTGGTGTCTGACCACTGCTACCCCTCTCGGGCGTGAACGAGACGAGGCTGGCC  
CTGCGCCCCCTGTATGATGACAGCCGAGCCATGGTCGGGCAAGCGCCAGGCCACTGCC  
CACTGCCCAACAGCTATGTTAATAACAATGACATCTACCAAGGTCACTCCTGCTACCGCCT  
CGGCTCCAACGACAAGGAGATCATGAAAGGAGCTGATGGAGAAATGGCCCTGCTCAAGCCCTCA  
TGGAGGTGCATGAGGACTTCTCCTATACAAGGGAGGCATCTACAGCCACAGCCAGTGAGC  
CTTGGGAGGCCAGAGAGATACGCCGCATGGACCCACTCAGTCAAGATCACAGGATGGGG  
AGAGGAGACGCTGCCAGATGAAAGGACGCTCAAATACTGGACTGCGGCCACTCCTGGGGCC  
CAGCCTGGGGCGAGAGGGCCACTTCCGCATCGTGCAGCGCGTCAATGAGTGCAGACATCGAG  
AGCTTGTGCTGGCGTCTGGGGCGCGTGGGATGGAGGACATGGGTATCACTGAGGCTG  
CGGGCACACGCCGGGTCCGGCCTGGGATCCAGGCTAAGGGCCGGCGGAAGAGGCCCAATG  
GGCGGTGACCCAGCCTGCCGACAGAGCCGGCGCAGGCGGGGCCAGGGCGCTAAT  
CCCAGCGGGTCTGGCTGACGCAGGCCCTGGAGGCCGGCAGGCGAGACTGGCG  
GAGCCCCAGACCTCCAGTGGGACGGGGCAGGGCTGGCTGGGAAGAGCACAGCTGCAG  
ATCCCAGGCCCTGGCGCCCCACTCAAGACTACCAAAGCCAGGACACCTCAAGTCTCCAGC  
CCCAATACCCACCCCAATCCGTATTCTTTTTTTTTAGACAGGGTCTGCTCCG  
TTGCCCAAGGTGGAGTGCAGTGGCCATCAGGGCTACTGTAACCTCCGACTCCTGGGTTCA  
AGTGCACCCCTCCACCTCAGCCTCTCAAGTAGCTGGACTACAGGTGCACCACACCTGGC  
TAATTTTGATTTTGTAAGAGGGGGTCTCACTGTGTTGCCAGGCTGGTTTCGAAC  
CCTGGGCTCAAGCGGTCCACCTGCCTCCGCTCCAAAGTGCAGGGATTGCAGGCATGAGCC  
ACTGCACCCAGCCCTGTATTCTTATTCTCAGATATTATTTCTTCACTGTTTAA  
TAAAACCAAAGTATTGATAAAAAAAA

## **FIGURE 6**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33223
><subunit 1 of 1, 164 aa, 1 stop
><MW: 18359, pI: 7.45, NX(S/T): 1
MWRCPLGLLLLLPLAGHLALGAQQGRGRRELAPGLHLRGIRDAGGRYCQEQLLCRGRADDC
ALPYLGAICYCDLFCNRTVSDCCPDFWDFCLGVPPPFPIQGCMHGGRIYPVLGTYWDNCNR
CTCQENRQWHGGSRHDQSHQPGQLWLAGWEPQRLLGHDPG
```

**N-glycosylation site.**

amino acids 78-82, 161-165

**Casein kinase II phosphorylation site.**

amino acids 80-84, 117-121, 126-130, 169-173, 205-209, 296-300,  
411-415

**N-myristoylation site.**

amino acids 21-27, 39-45, 44-50, 104-110, 160-164, 224-230,  
269-275, 378-384, 442-448

**Amidation site.**

amino acids 26-30, 318-322

**Eukaryotic thiol (cysteine) proteases histidine active site.**

amino acids 398-409

## **FIGURE 7**

AGGCTCCTGGCCCTTTCCACAGCAAGCTNTGCNATCCGATTGTTGTCTCAAATCCA  
ATTCTCTTGGGACACATNACGCCTGTCCTTNGCCCCAGAACCTGCTGTCTGTACACCCAC  
CAGCAGCAGGGCTGCCCGNTGGCGTCTCGATGGTGCTGGTGGTCCCTGCGTCGCCGAGG  
GNTGGTGTCTGACCACTGCTACCCCTCTCGGGCGTGAACGAGACGAGGCTGGCCCTGCGC  
CCCCCTGTATGATGCACAGCCGAGCCATGGTCGGGGCAAGGCCAGGCCACTGCCACTGC  
CCCAACAGCTATGTTAATAACAATGACATCTACCAAGGTCACTCCTGTCTACCGCCTCGGCTC  
CAACGACAAGGAGATCATGAAGGAGCTGATGGAGAATGGCCCTGTCCAAGCCCTATGGAGG  
TGCATGAGGACTTCTCCTATACAAGGGAGGCATCTACAGCCACAGCCAGTGAGCCTGGG  
AGGCCAGAGAGATAACGCCGGCATGGGACCCACTCAG

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## **FIGURE 8**

GCTGCTGCCCTGTTGATGGCAGGCTGGCCCTGCAGCCAGGCACTGCCCTGCTGTGCTACT  
CCTGCAAAGCCCAGGTGAGCAACGAGGACTGCCTGCAGGTGGAGAACTGCACCCAGCTGGGG  
GAGCAGTGCTGGACCGCGCATCCGCGCAGTTGGCCTCTGACCGTCATCAGCAAAGGCTG  
CAGCTGAACTGCGTGG**AT**GACTCACAGGACTACTACGTGGCAAGAAGAACATACGTGCT  
GTGACACCGACTTGTGCAACGCCAGCGGGCCATGCCCTGCAGCCGGCTGCCGCATCCTT  
GCGCTGCTCCCTGCACTCGGCCTGCTGCTCTGGGGACCCGGCCAGCTATAAGGCTCTGGGGGG  
CCCCGCTGCAGCCCACACTGGGTGTGGTCCCCAGGCCTCTGTGCCACTCCTCACAGACCTG  
GCCCAAGTGGGAGCCTGTCCTGGTTCCCTGAGGCACATCCTAACGCAAGTCTGACCATGTATGT  
CTGCACCCCTGTCCCCACCCCTGACCCCTCCATGCCCTCTCCAGGACTCCCACCCGGCAGA  
TCAGCTCTAGTGACACAGATCCGCCTGCAGATGCCCTCCAACCCCTCTGCTGCTGTTTC  
CATGGCCCAGCATTCTCCACCCCTAACCCCTGTGCTCAGGCACCTCTCCCCAGGAAGCCTT  
CCCTGCCACCCATCTATGACTTGAGCCAGGTCTGGTCCGTGGTGTCCCCCGCACCCAGCA  
GGGGACAGGCACTCAGGAGGGCCCAG**TAA**AGGCTGAGATGAAGTGGACTGAGTAGAAACTGGA  
GGACAAGAGTCGACGTGAGTTCCCTGGGAGTCTCCAGAGATGGGCCTGGAGGCCTGGAGGAA  
GGGGCCAGGCCTCACATTGTTGGCTCCCTGAATGGCAGCCTGAGCACAGCGTAGGCCCTT  
AATAAACACCTGTTGGATAAGCCAAAAAA

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## **FIGURE 9**

MTHRTTWARRTSRAVTPTCATPAGPMPCSRLPPSLRCSLHSACCSGDPASYRLWGAPLQPT  
LGVVPQASVPLLTDLAQWEPVLVPEAHPNASLTMYVCTPVPHPDPPMALSRTPTRQISSLDT  
DPPADGPSNPLCCCFFHGPAGFSTLNPVLRHLFPQEAFPAHPIYDLSQVWSVVSPAPSRGQALRRAQ

**Signal peptide:**

amino acids 1-47

**N-glycosylation site.**

amino acids 31-35, 74-78, 84-88

**Casein kinase II phosphorylation site.**

amino acids 22-26, 76-80

**N-myristoylation site.**

amino acids 56-60

**Amidation site.**

amino acids 70-74

## **FIGURE 10**

CCACCGCGTCCGAAACCTCTCCAGCGAGGGAGCCGCCGCTGCTGCCAACCTCACTCTGT  
GCTTACAGCTGCTGATTCTCTGCTGTCAAACACTCAGTACGTGAGGGACCAGGGGCCATGACC  
GACCAGCTGAGCAGGCGGCAGATCCGCGAGTACCAACTCTACAGCAGGACCAGTGGCAAGCA  
CGTGCAGGTCAACGGGCGTCGCATCTCCGCCACGCCGAGGACGGCAACAAGTTGCCAAGC  
TCATAGTGGAGACGGACACGTTGGCAGCCGGGTTGCATCAAAGGGCTGAGAGTGAGAAG  
TACATCTGTATGAACAAGAGGGCAAGCTCATCGGAAGCCCAGCGGGAAAGAGCAAAGACTG  
CGTGGTCACGGAGATCGTGGAGAACAACTATAACGCCCTCCAGAACGCCGGCACGAGG  
GCTGGTTCATGGCCTTCACGCCGCAGGGCGGCCAGGCTTCCGCAGGCCAGAAC  
CAGCGCGAGGCCCACTTCATCAAGGCCCTCTACCAAGGCCAGCTGCCCTCCCCAACACGC  
CGAGAACAGAAGCAGTCGAGTTGTGGCTCCGCCACCCGCCGACCAAGCGCACAC  
GGCGGCCCAAGCCCTCACGTAGTCTGGGAGGCAGGGGCAGCAGCCCTGGCCGCCTCCC  
CACCCCTTCCCTTAACTCAAGGACTGGCTGGGTGGCGGGAGGGGAGCCAGATCCCC  
GAGGGAGGACCCCTGAGGCCCGAAGCATCCGAGCCCCCAGCTGGGAAGGGCAGGCCGGTGC  
CCCCAGGGCGGCTGGCACAGTGCCCTCCGGACGGTGGCAGGCCCTGGAGAGGAAC  
GAGTGTACCCCTGATCTCAGGCCACCAGCCTGCGGCCCTCCAGCCGGCTCCTGAAGCC  
CGCTGAAAGGTCAAGCGACTGAAGGCCTTGCAGACAACCGTCTGGAGGTGGCTGTCCCTCAAAA  
TCTGCTTCTCGGATCTCCCTCAGTCTGCCCTCAGGAAACCTCCTGGCTAGACTGTA  
GGAAGGGACTTTGTTGTTGTTGTTCAAGAAAAAGAAAGGGAGAGAGAGGAAAATAG  
AGGGTTGTCCACTCCTCACATTCCACGACCCAGGCCTGCACCCACCCCCACTCCAGCCC  
CGGAATAAAACCATTTCTGC

## **FIGURE 11**

MGAARLLPNLTLCLQLLILCCQTQYVRDQGAMTDQLSRRQIREYQLYSRTSGKHVQVTGRRI  
SATAEDGNKFAKLIVETDTFGSRVRIKGAESEKYICMNNKRGKLIGKPSGSKDCVFTEIVLE  
NNYTAFQNARHEGWFMAFTRQGRPRQASRSRQNQREAHFIKRLYQGQLPFPNHAEKQQQFEEF  
VGSAPTRRTKRTRRPQPLT

**Signal peptide:**

amino acids 1-22

**N-glycosylation site.**

amino acids 9-13, 126-130

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 60-64

**Casein kinase II phosphorylation site.**

amino acids 65-69

**Tyrosine kinase phosphorylation site.**

amino acids 39-48, 89-97

**N-myristoylation site.**

amino acids 69-75, 188-194

**Amidation site.**

amino acids 58-62

**HBGF/FGF family signature.**

amino acids 103-128

## **FIGURE 12**

ACTTGCCATCACCTGTTGCCAGTGTGGAAAATTCTCCCTGTTGAATTTCATGGAG  
GACAGCAGCAAAGAGGGCAACACAGGCTGATAAGACCAAGAGACAGCAGGGAGATTATTTAC  
CATACGCCCTCAGGACGTTCCCTCTAGCTGGAGTTCTGGACTTCAACAGAACCCCATCCAGT  
CATTGATTTGCTGTTATTTTTCTTTCTTTCCCACCAATTGTATTTAT  
TTCCGTACTTCAGAA**AT**GGGCCTACAGACCACAAAGTGGCCAGCCATGGGCTTTCT  
GAAGTCTGGCTTATCATTCCCTGGGGCTCTACTCACAGGTGTCAAACCTCTGGCCTGCC  
CTAGTGTGTGCCGCTGCGACAGGAACCTTGTCTACTGTAATGAGCGAAGCTGACCTCAGTG  
CCTCTGGGATCCCAGGGCGTAACCGTACTCTACCTCCACAACAACCAAATTAAATAATGC  
TGGATTCCTGCAGAACTGCACAATGTACAGTCGGTGACACGGCTACCTGTATGGCAACC  
AACTGGACGAATTCCCCATGAACCTTCCAAGAAATGTACAGGTTCTCCATTGCAGGAAAC  
AATATTGAGACCAATTTCACGGCTGCTTGCCCCAGCTTGAAGCTGAAGAGCTGCACCT  
GGATGACAACCTCCATATCCACAGTGGGGTGGAAAGACGGGCCTCCGGGAGGCTATTAGCC  
TCAAATTGTTGTTTGTCTAAGAATCACCTGAGCAGTGTGCCCTGGCTTCCGTGGAC  
TTGCAAGAGCTGAGAGTGGATGAAAATCGAATTGCTGTATATCCGACATGGCCTCCAGAA  
TCTCACGAGCTGGAGCGTCTTATTGTGGACGGAACCTCCTGACCAACAAAGGTATGCCG  
AGGGCACCTTCAGCCATCTCACCAAGCTCAAGGAATTTCATATTGTACGTAATTGCTGTCC  
CACCCCTCCTCCCGATCTCCAGGTACGCATCTGATCAGGCTCTATTGCAGGACAACAGAT  
AAACACATTCTTGACAGCCTCTCAAATCTCGCTAACGCTGGATATATCCA  
ACAACCAACTGCGGATGCTGACTCAAGGGTTTGATAATCTCTCCAAACCTGAAGCAGCTC  
ACTGCTCGGAATAACCCCTGGTTTGACTGCAGTATTAAATGGGTACAGAAATGGCTCAA  
ATATATCCCTCATCTCAACGTGCGGGTTCATGTGCCAAGGTCTGAACAAAGTCCGG  
GGATGGCGTCAGGGAAATTAAATATGAATCTTGTCCCTGCCCACCGACCCCCGGCCTG  
CCTCTCTCACCCAGCCCCAAGTACAGCTCTCCGACCAACTCAGCCTCCACCCCTCTAT  
TCCAAACCTAGCAGAAGCTACAGCCTCCAACCTTACACATCGAAACTTCCCACGATT  
CTGACTGGGATGGCAGAGAAAGAGTGAACCCACCTATTCTGAACGGATCCAGCTCTATC  
CATTGTTGAAATGATACTTCAAGTCAGCTGGCTCTCTCTTCAACCGTGATGGCATA  
CAAACTCACATGGGTAAAATGGGCCACAGTTAGTAGGGGGCATCGTTCAGGAGCGCATAG  
TCAGCGGTGAGAAGCAACACCTGAGCCTGGTTAACTTAGAGCCCCGATCCACCTATCGGATT  
TGTTAGTGCCACTGGATGCTTTAACTACCGCGCGGTAGAAGACACCATTGTTAGAGGC  
CACCACCCATGCCTCTATCTGAACACGGCAGCAACACAGCGTCCAGCCATGAGCAGACGA  
CGTCCCACAGCATGGCTCCCCCTTCTGCTGGCGGGCTTGATGGGGCGCGGTGATATT  
GTGCTGGTGGTCTTGCCTCAGCGTCTTGTGCATATGCACAAAAGGGCGCTACACCTC  
CCAGAAGTGGAAATACAACCGGGCGGGAAAGATGATTATTGCGAGGCAGGCACCAAGA  
AGGACAACCTCCATCTGGAGATGACAGAAACCAGTTTCAGATCGTCTCCTAAATAACGAT  
CAACTCCTAAAGGAGATTCAAGACTGCAGCCATTACACCCCAAATGGGGCATTAAATTA  
CACAGACTGCCATATCCCCAACACATGCGATACTGCAACAGCAGCGTGCCAGACCTGGAGC  
ACTGCCATACGTGACAGCCAGAGGCCAGCGTTATCAAGGCGGACAATTAGACTCTTGAGAA  
CACACTCGTGTGTCACATAAAGACACGCAGATTACATTGATAAAATGTTACACAGATGCAT  
TTGTCATTGAAACTCTGTAATTACGGTGTACTATATAATGGGATTAAAAAAAGTG  
CTATTTCTATTCAAGTTAAATTACAAACAGTTGTAACCTTTGCTTTAAATCTT

## **FIGURE 13**

MGLQTTKWPShGaffFLKSwLIISLGLYSQVSKLLACPSVCRCDRNFVYCNERSLTSVPLGIP  
EGVTvLYLHNNQINNAGFPaELHNVQSVHTVYLYGNQLDEFPMNLPKNVRVLHLQENNIQTI  
SRAALAQLLKLEELHLDdnsISTVGVEDGAFREAIISLKLFLSKNHLSSVPVGLPVDLQELR  
VDENRIAVISDMAFQNLTSLERLIVDGNLLTNKGIAEGTFSHLTKLKEFSIVRNSLSHPPPD  
LPGTHLIRLYLQDNQINHIPLTAFSNLRKLERLDISNNQLRMLTQGVFDNLSNLKQLTARN  
PWFCDCSIKWVTEWLKYIPSSLNVRGFMCGPEQVRGMAVRELMNLLSCPTTPGLPLFTP  
APSTASPTTQPPTLSIPNPSRSYTPPTPTSKLPTIPDWDGRERVTppISERIQLSIHFVND  
TSIQVSWLSLFTVMAyKLTWVKGHSIVGGIVQERIVSGEKQHLSLVNLEPRSTYRICLVPL  
DAFNYRAVEDTICSEATTHASyLNNGSNTASSHEQTTSHSMGSPFLLAGLIGGAVIFVLVVL  
LSVFCWHMHKKGRYTSQKWKYNRGRRKDDYCEAGTKKDnsILEMTEtsFQIVSLNNNDQLLKG  
DFRLQPIYTPNGGINYTDCHIPNNMRYCNSSVPDLEHCHT

**Signal peptide:**

amino acids 1-42

**Transmembrane domain:**

amino acids 542-561

**N-glycosylation site.**

amino acids 202-206, 298-302, 433-437, 521-525, 635-639, 649-653

**Casein kinase II phosphorylation site.**

amino acids 204-208, 407-411, 527-531, 593-597, 598-602, 651-655

**Tyrosine kinase phosphorylation site.**

amino acids 319-328

**N-myristoylation site.**

amino acids 2-8, 60-66, 149-155, 213-219, 220-226, 294-300,  
522-528, 545-551, 633-639

**Amidation site.**

amino acids 581-585

**Leucine zipper pattern.**

amino acids 164-186

**Phospholipase A2 aspartic acid active site.**

amino acids 39-50

## FIGURE 14

ACTTGGAGCAAGCGCGGGCGGAGACAGAGGCAGAGGCAGAAGCTGGGCTCCGCTCGCCTCCACGAGCG  
ATCCCCGAGGAGAGCCGCGCCCTCGGCAGGGCGAAGAGGCGACGAGGAAGACCCGGGTGGCTCGGCCCTGCC  
TCGCTTCCCAGGCAGCCGGCTGAGCCTTGCCTCCCTGGCTGAGGGCAGGGAGCGGTACGTGGAGGTCCATCT  
CTAGGGCAGACACGCTCGGACCCACCCGAGACGGCCCTCTGGAGAGTCTCTGTAGAAAGAGTCAAGGAGTTCATCGTGGACA  
TGGTTTCATCATTGACAGCTCTCGCAGTGTCAACACCCATGACTATGCAAGAGTCAGGAGTTCATCGTGGACA  
TCTTGCATTCTGGACATTGGTCTGTGTCACCCGAGTGGGCTGCTCAATATGGCAGCACTGTCAAGAATG  
AGTTCTCCCTCAAGACCTCAAGAGGAAGTCCGAGGTGGAGCTGTCAAGAGGATGCGGCATCTGTCCACGG  
GCACCATGACTGGCTGGCCATCCAGTATGCCCTGAACATCGCATTCTCAGAAGCAGAGGGGGGGGGGGGG  
GGGAGAATGTGCCACGGGTCAATAATGATCGTACAGATGGAGACCTCAGGACTCCGTGGCCAGGGTGGCTGCTA  
AGGCACGGGACACGGGCATCTTAATCTTGCCATTGGTGTGGCCAGGTAGACTTCAACACCTGAAGTCCATTG  
GGAGTGAGCCCCATGAGGACCATGTCTCCTTGTGGCAATTCAAGCCAGATTGAGACGCTGACCTCCGTGTTCC  
AGAAGAAGTTGTGACGGCCACATGTGAGCAGCACCTGGAGCATAACTGTGCCACTCTGCATCAACATCCCTG  
GCTCATACGTCTGCAGGTGAAACAAGGCTACATTCTCAACTCGGATCAGACGACTTGAGAATCCAGGATCTGT  
GTGCCATGGAGGACCAACTGTGAGCAGCTGTGTGAATGTGCCGGCTCTCGTGTGCACTGAGTACAGT  
GCTACGCCCTGGCTGAGGATGGGAAGAGGTGTGGACTACTGTGCCCTAGAAAACCACGGATGTGAAC  
ATGAGTGTGAAATGCTGATGGCTCTACCTTGCCAGTGCATGAAGGATTGCTCTTAACCCAGATGAAAAAA  
CGTGACAAGGATCAACTACTGTGCACTGAACAAACCGGGCTGTGAGCATGAGTGCCTCAACATGGAGGAGAGCT  
ACTACTGCCGCTGCCACCGTGGCTACACTCTGGACCCAAATGGAAAACCTGCAGCCAGTGGACCACTGTGCAC  
ACGAGGACCATGGCTGTGAGCAGCTGTGTGAACACCGAGGATTCTCGTGTGCAAGGGCTCAGAAGGCTTCC  
TCATCAACGAGGACCTCAAGACCTGCTCCGGGTGGATTACTGCCCTGCTGAGTGACCATGGTTGTGAATACTCCT  
GTGTCACATGGACAGATCCTTGCTCTGCACTGTGCTGAGGGACACGTGCTCCGCAGCGATGGGAAGACGTGTG  
CAAATGGACTCTTGTGCTCTGGGGGACACGGTTGTGAACATTGTGTGAAGCAGTGAAGATTGTTGTG  
GCCAGTGTGTTGAAGGTTATATACTCCGTGAAGATGGAAAACCTGCAGAAGGAAAGATGTCTGCCAAGCTATAG  
ACCATGGCTGTGAACACATTGTGAACAGTGCAGACTCATACACGTGCGAGTGTGCTGGAGGGATTCCGGCTCG  
CTGAGGATGGGAACACGCTGCCGAAGGAAGGATGTCTGCAATCAACCCACATGGCTGCCAACACACATTGTGTTA  
ATAATGGGAATTCTACATCTGCAAAATGCTCAGAGGGATTGTTCTAGCTGAGGAGCGGAAGACGGTGCAAGAAAT  
GCACTGAAGGCCAATTGACCTGGTTGTGATGGATCCAAGAGTCTGGAGAAGAGAATTGGAGGTG  
TGAAGCAGTTGTCACTGAAATTATAGATTCTTGACAATTTCACCGTGTGAGTGGGGCTGCTCCAGT  
ATTCCACACAGGTCCACACAGAGTTCACTCTGAGAAACCTCAACTCAGCAAAGACATGAAAAAAGCCGTGGCCC  
ACATGAAATACATGGGAAGGGCTATGACTGGCTGCCCTGAAACACATGTTGAGAGAAGTGGTACCAAG  
GAGAAGGGGCCAGGCCCTTCCACAAGGGTGCCAGACCGAGCCATTGTTGACCGACGGACGGGCTCAGGATG  
ACGTCCTGGAGTGGGCCAGTAAAGCCAAGGCCAATGGTATCACTATGTATGCTGTTGGGGTAGGAAAAGCCATTG  
AGGAGGAACATACAAGAGATTGCCCTGAGCCCACAAACAAGCATCTTCTATGCCGAAGACTTCAGCACAATGG  
ATGAGATAAGTAAAAACTCAAGAAAGGCATCTGTGAAGCTCTAGAAGACTCCGATGGAAGACAGGACTCTCCAG  
CAGGGAACTGCCAAAAACGGTCCAACAGCCAACAGAAATCTGAGCCAGTCACCATAAATATCCAAGACCTACTTT  
CTGTTCTAATTTCAGTGCAACACAGATATCTGTTGAAGAAGACAATCTTACGGTCTACACAAAGCTTT  
CCCATTCAACAAACCTCAGGAAGGCCCTTGGAAAGAAAAACAGATCAATGCAAATGAAACCTTATAATGT  
TCCAGAACCTTGCACAGAAGAAGTAAAGAAAATTAAACACAGCGCTTAGAAGAAATGACACAGAGAATGGAAGGCC  
TGGAAAATGCCCTGAGATAACAGATGAAGATTAGAAATCGCAGACACATTGAGTCTATTGTATCACGGATTACAAT  
GAACCGAGTGCAGAGGCCAAAGCTCAGGCTATTGTTAAATCAATAATGTTGTGAAGTAAACAAATCAGTACTGA  
GAAACCTGGTTGCCACAGAACAAAGACAAGAAGTATACTACTAATGTTGAGTAAATTTATCTAGGAAAAAAATCCT  
TCAGAATTCTAAGATGAATTACCAAGGTGAGAATGAATAAGCTATGCAAGGTATTGTAATATACTGTGGACAC  
AACTTGCTCTGCCCTACCTGCCCTAGTGTGCAATCTCATTGACTATACGATAAAAGTTGCACAGTCTTACTT  
CTGAGAACACTGCCATAGGAAATGCTGTTTTGTACTGGACTTACCTTGATATGTATATGGATGTATG  
CATAAAATCATAGGACATATGTACTTGTGGAACAAGTGGATTTTATACAATATAAAATTCAACTTCAG

## **FIGURE 15**

MEKMLAGCFLLILGQIVLLPAEARERSRGRSISRGHRARTHPOQTALLESSCENKRADLVFII  
DSSRSVNTHDYAKVKEFIVDILQFLDIGPDVTRVGLLQYGSTVKNEFSLKTFKRKSEVERAV  
KMRHLSTGTMGLAIQYALNIAFSEAE GARPLREN VPRVIMIVTDGRPQDSVAEVAAKARD  
TGILIFIAIGVGQVDFNTLKSIGSEPHEDHVFLVANFSQIETLTSVFQKKLCTAHMCSTLEHN  
CAHFCINIPGSYVCRCKQGYILNSDQTTCRIQDLCAMEDHNCEQLCVNVPGSFVCQCYSGYA  
LAEDGKRCVAVDYCASENHGCEHECVNADGSYLCQCHEGFALNPDEKTCTRINYCALNKG  
EHECVNMEESYYCRCHRGYTLDPNGKTCRVDHCAQQDHGCEQLCLNTEDSFVCQCSEGFLI  
NEDLKTCSRVDYCLLSDHGCEYSCVNMDRSFACQCPEGHVLRS DGKTCAKLDSCALGDHGCE  
HSCVSSEDSFVCQCFCFGYILREDGKTCRVDHCAQQDHGCEQLCLNTEDSFVCQCSEGFLI  
EDGKRCRCKDVCKSTHGCEHICVNNNGNSYICKCSEGFLAEDGRRCKCTEGPIDLVFVID  
GSKSLGEENFEVVVKQFVTGIIDSLTISPKAARVGLLQYSTQVHTEFTLRFNSAKDMKKAVA  
HMKYMGKGSMTGLALKHMFERSFTQGEGARPLSTRVPRAAIVFTDGRAQDDVSEWASKAKAN  
GITMYAVGVGKAIEEELQEIASEPTNKHLYAEDFSTMDEISEKLKGICEALEDSDGRQDS  
PAGELPKTVQQPTESEPVTINIQDLLSCSNFAVQHRYLFEEDNLLRSTQKLSHSTKPSGSPL  
EEKHDQCKCENLIMFQNLANEEVRKLTQRLEEMTQRMEALENRLRYR

**Signal peptide:**

amino acids 1-23

**N-glycosylation site.**

amino acids 221-225

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 115-119, 606-610, 892-896

**Casein kinase II phosphorylation site.**

amino acids 49-53, 118-122, 149-153, 176-180, 223-227, 243-247,  
401-405, 442-446, 501-505, 624-628, 673-677, 706-710, 780-784,  
781-785, 819-823, 866-870

**N-myristoylation site.**

amino acids 133-139, 258-264, 299-305, 340-346, 453-459, 494-500,  
639-645, 690-696, 752-758, 792-798

**Amidation site.**

amino acids 314-318, 560-564, 601-605

**Aspartic acid and asparagine hydroxylation site.**

amino acids 253-265, 294-306, 335-347, 376-388, 417-423, 458-464,  
540-546, 581-587

## **FIGURE 16**

GGAGCCGCCCTGGGTGTCAGCGCTCGGCTCCCGCGCACGCTCCGGCGTCGCAGCCTCG  
GCACCTGCAGGTCCGTGCGTCCCGCGCTGGCGCCCGTACTCCGTCCCGCCAGGGAGGGC  
**CATG**ATTCCTCCCTCCGGGCCCCCTGGTGACCAACTTGCTGCGGTTTTGTTCTGGGCTGA  
GTGCCCTCGCGCCCCCTCGCGGGCCAGCTGCAACTGCACCTGCCGCCAACCGGTTGCAG  
GCGGTGGAGGGAGGGAAAGTGGTGCTTCCAGCGTGGTACACCTGCACGGGAGGGTGTCTTC  
ATCCCAGCCATGGGAGGTGCCCTTGATGTGGTCTTCAAACAGAAAGAAAAGGAGGATC  
AGGTGTTGTCCTACATCAATGGGTACAACAAGCAAACCTGGAGTATCCTGGTCTACTCC  
ATGCCCTCCCGAACCTGTCCCTGCCAGCTCCAGCTCCATCCTGCCGTCTCAGGGTGTGCCCTA  
CAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGGGCCACAGCATAAAACCT  
TAGAACTCAATGTACTGGTTCTCCAGCTCCATCCTGCCGTCTCAGGGTGTGCCCTA  
GTGGGGCAAACGTGACCCCTGAGCTGCCAGTCTCCAAGGAGTAAGCCCGCTGTCCAATACCA  
GTGGGATCGGCAGCTCCATCCTCCAGCTTCTTGCACCAGCATTAGATGTCATCCGTG  
GGTCTTAAGCCTACCAACCTTCGTCTCCATGGCTGGAGTCTATGTCTGCAAGGCCAC  
AATGAGGTGGGCACTGCCAATGTAATGTGACGCTGGAAGTGAGCACAGGGCTGGAGCTGC  
AGTGGTTGCTGGAGCTGTTGTTGGTACCCCTGGTGGACTGGGGTTGCTGGCTGGCTGGTCC  
TCTTGTACCACCGCCGGCAAGGCCCTGGAGGAGCCAGCCAATGATATCAAGGAGGATGCC  
ATTGCTCCCCGGACCCCTGCCCTGCCCAAGAGCTCAGACACAATCTCAAGAATGGGACCC  
TTCCTCTGTCACCTCCGCACGAGCCCTCCGGCCACCCCATGCCCTCCAGGCCTGGTGCAT  
TGACCCCCACGCCAGTCTCCAGCCAGGCCCTGCCCTCACCAAGACTGCCACGACAGAT  
GGGGCCCACCCCTCAACCAATATCCCCATCCCTGGTGGGTTCTCCTCTGGCTTGAGCCG  
CATGGGTGCTGTGCCTGTGATGGTGCCCTGCCAGAGTCAGACTGGCTCTGGTAT**GATGAC**  
CCCACCACTATTGGCTAAAGGATTGGGAAAGAGTCACACTCCTGACCCCTAGTACTCTGCC  
AGAGGCCTGAGTCATGGAAAGAGTCACACTCCTGACCCCTAGTACTCTGCC  
TTTACTGTGGAAAACCCTCACTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGA  
AGTGGATCTGGAATTGGGAGGAGCCTCCACCCACCCCTGACTCCTCCTTATGAAGCCAGCTG  
CTGAAATTAGCTACTCACCAAGAGTGAGGGCAGAGACTCCAGTCAGTCAAGTCTCCAGGC  
CCCCCTGATCTGTACCCACCCCTATCTAACACCACCCCTGGCTCCACTCCAGCTCC  
ATTGATATAACCTGTCAGGCTGGCTGGTTAGGTTTACTGGGGCAGAGGATAGGAAATCTC  
TTATTAACATGAAATATGTGTTTTCAATTGCAAATTAAATAAGATAACATAA  
TGTTGTATGAAAAA

## **FIGURE 17**

MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEVSS  
SQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKDGPY  
SCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHGANVTLSCQSPRSKPAVQYQ  
WDRQLPSFQTFFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTACQCVTLEVSTGPGAA  
VVAGAVVGTIVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLWPWPKSSDTISKNGTL  
SSVTSARALRPPHGPPRPGALTPTPSLSSQALPSPRLPTTDGAHPQPISPIPGGVSSSGLSR  
MGAVPVMVPAQSQAGSLV

**Signal peptide:**

amino acids 1-29

**Transmembrane domain:**

amino acids 245-267

**N-glycosylation site.**

amino acids 108-112, 169-173, 213-217, 236-240, 307-311

**N-myristoylation site.**

amino acids 90-96, 167-173, 220-226, 231-237, 252-258, 256-262,  
262-268, 308-314, 363-369, 364-370

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 164-175

## FIGURE 18

CGCCACCACTCGGGCACCGCCAATGAAACGCCTCCGCTCTAGGGTTTTCCACTTTG  
TTGAATTGTCCTATACTCAAAATTGCAACAGACACCTGTCTCCAAATGAAAATGTGA  
AATACGCAATGGAATTGAGCCTGCTATTGCAACATGGGATTTCAGGAAATGGTGTACAA  
TTTGTGAAGATGATAATGAATGTGGAAATTAACTCAGTCCTGTGGCAAATGCTAATTGC  
ACTAACACAGAAGGAAGTTATTATTGTATGTGTACCTGGCTCAGATCCAGCAGTAACCA  
AGACAGGTTATCACTAATGATGGAACCGTCTGTATAGAAAATGTGAATGCAAACGCCATT  
TAGATAATGTCTGTATAGCTGCAAATATTAAATAAAAACCTTAACAAAAATCAGATCCATAAAA  
GAACCTGTGGCTTGCTACAAGAAGTCTATAGAAATTCTGTGACAGATCTTCACCAACAGA  
TATAATTACATATATAGAAATTAGCTGAATCATCTTCATTACTAGGTTACAAGAACAA  
CTATCTCAGCCAAGGACACCCCTTCTAACTCAACTCTTAAGGATATGGTAAACCGTGAAT  
AATTTGTTCAAAGGGATACATTGTAGTTGGACAAGTTATCTGTGAATCATAGGAGAAC  
ACATCTTACAAAACATGCACACTGTTGAACAAGCTACTTTAAGGATATCCCAGAGCTTCC  
AAAAGACCACAGAGTTGATACAAATTCAACGGATATAGCTCTCAAAGTTTCTTTGAT  
TCATATAACATGAAACATATTCACTCCTCATATGAATATGGATGGAGACTACATAAATATT  
TCCAAAGAGAAAAGCTGCATATGATTCAAATGGCAATGTTGAGTTGCATTTCATTTATATT  
AGAGTATTGGTCCTTGCTTCATCATCTGACAACCTTCTTATTGAAACCTCAAATTATGAT  
AATTCTGAAGAGGGAGGAAAGAGTCATATCTTCAGTAATTTCAGTCTCAATGAGCTCAAACCC  
ACCCACATTATATGAACATTGAAACATTACATTACATTAAAGTCATCGAAAGGTACAGATA  
GGTATAGGAGTCTATGTGCATTGGAAATTACTCACCTGATACCATGAATGGCAGCTGGTCT  
TCAGAGGGCTGTGAGCTGACATACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCT  
GACACATTGCAATTGATGTCCTCTGGCCTTCATTGGTATTAAAGATTATAATATT  
TTACAAGGATCACTCAACTAGGAATAATTATTCACTGATTGCTTGCCATATGCATTTT  
ACCTTCTGGTCTTCAGTCAAAGCACCAGGACAACAATTCAACAAAATCTTGCTG  
TAGCCTATTCTTGCTGAATTGTTCTTGTGGATCAATACAAATACTAATAAGCTCT  
TCTGTTCAATCATTGCCGACTGCTACACTACTTCTTAGCTGCTTGCATGGATGTGC  
ATTGAAGGCATACATCTATCTATTGTTGGCTATCTAAGGCCAGCCGTGGTAGTTGGATTTCGGCAGCAC  
TAGGATACAGATATTATGGCACAACCAAGTATGTTGGCTTAGCACCAAAACAACATT  
TGGAGTTTATAGGACCAGCATGCCTAATCATCTTGTAAATCTCTGGCTTGGAGTCAT  
CATATACAAAGTTTCTGTCACACTGCAGGGTTGAAACCAGAAGTTAGTGTCTTGAGAAC  
TAAGGTCTGTGCAAGAGGGAGCCCTCGCTCTCTGTTCTCGGCACCACCTGGATCTT  
GGGGTCTCCATGTTGTGCACGCATCAGGTTACAGCTTACCTCTCACAGTCAGCAATGC  
TTTCAGGGATGTTCATTTTATTCCTGTGTTTATCTAGAAAGATTCAAGAAGAAT  
ATTACAGATTGTTAAAAATGCCCCGTTGGATGTTAAGGTAACATAGAGAATG  
GTGGATAATTACAACGTGACAAAAATAAAATTCAAGCTGTGGATGACCAATGTATAAAA  
TGACTCATCAAATTATCAATTAAACTACTAGACAAAAAGTATTAAATCAGTTTCT  
GTTATGCTATAGGAACGTGAGATAATAAGGAAAATTATGTATCATATAGATATACTATGT  
TTTCTATGTGAAATAGTTCTGTCAAAATAGTATTGCAAGATATTGGAAAGTAATTGGTT  
CTCAGGAGTGTATCACTGCACCCAGGAAAGATTCTTCTAACACAGAGAAGTATATGAA  
TGTCTGAAGGAAACCACTGGCTGATATTCTGTGACTCGTGTGCCTTGAAACTAGTCC  
CCTACCACTCGTAATGAGCTCCATTACAGAAAGTGGAACATAAGAGAATGAAGGGCAGA  
ATATCAAACAGTGAAAGGGATGATAAGATGTATTTGAATGAACTGTTTCTGTAGAC  
TAGCTGAGAAATTGTTGACATAAAATAAGAATTGAAGAACACATTTCACCATTGTGAA  
TTGTTCTGAACCTAAATGTCCACTAAAACAACCTAGACTCTGTTGCTAAATCTGTTCTT  
TTCTAATATTCTAAAAAAAGGTTACCTCCACAAATTGAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 19**

MKRLPLLVFSTLLNCSYTQNCTKTPCLPNAKCEIRNGIEACYCNMGFSGNGVTICEDDNEC  
GNLTQSCGENANCTNTEGSYYCMCVPGFRSSSNQDRFITNDGTVCIENVANCHLDNVCIAA  
NINKTLTKIRSIKEPVALLQEYVRNSVTDLSPTDIITYIEILAESSSLGYKNNTISAKDTL  
SNSTLTFVKTVNPFVQRDTFVWDKLSVNRRTHLTLMHTVEQATLRIQSFKTTEFDT  
NSTDIALKVFVFFDSYNMKHIHPHMNMDGYINIFPKRKAAYDSNGNVAVAFLYYKSIGPLLS  
SSDNFLLPQNYDNSEEERVISSVISVSMSSNPPTLYELEKITFTLSHRKVTDRYRSLCAF  
WNYS PDTMNGSWSSEGCELTYSNETHTSCRCNLTHFAILMSSGPSIGIKDYNILTRITQLG  
IIISLICLAI CIFTFWFSEIQSTRTTIHKNLCCSLFLAELVFLVGINTNTNKLFC SIIAGL  
LHYFFLAFAFWMCIEGIHLYLIVVGVIYNKGFLHKNFYIFGYLSPAVVVGFSAA LGYRYYGT  
TKVCWLSTENNFIWSFIGPACLIILVNLLAFGVIIYKVFRHTAGLKPEVSCFENIRSCARGA  
LALLFLLGTTWIFGVVLHVHASVVTAYLFTVSNAFQGMFIFLFLCVLSRKIQEEYYRLFKNV  
PCCFGCLR

**Signal peptide:**

amino acids 1-19

**Transmembrane domain:**

amino acids 430-450, 465-486, 499-513, 535-549, 573-593, 619-636,  
648-664

**N-glycosylation site.**

amino acids 15-19, 21-25, 64-68, 74-78, 127-131, 177-181,  
188-192, 249-253, 381-385, 395-399

**Glycosaminoglycan attachment site.**

amino acids 49-53

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 360-364

**Casein kinase II phosphorylation site.**

amino acids 54-58, 68-72, 76-80, 94-98, 135-139, 150-154,  
155-159, 161-165, 181-185, 190-194, 244-248, 310-314, 325-329,  
346-350, 608-612

**Tyrosine kinase phosphorylation site.**

amino acids 36-44, 669-677, 670-678

**N-myristoylation site.**

amino acids 38-44, 50-56, 52-58, 80-86, 382-388, 388-394,  
434-440, 480-486, 521-527

**Aspartic acid and asparagine hydroxylation site.**

amino acids 75-87

## **FIGURE 20**

TGGAAACATATCCTCCCTCATATGAATATGGATGGAGACTACATAAATATTTCCAAAGNG  
AAAAGCCGGCATATGGATTCAAATGGAATGTTGCAGTGATTTATATTATAAGAGTAT  
TGGTCCCTTGCTTCATCATCTGACAACCTCTTATTGAAACCTCAAAATTATGATAATTCT  
GAAGAGGAGGAAAGAGTCATATCTTCAGTAATTCAGTCTCAATGAGCTCAAACCCACCCAC  
ATTATATGAACTTGAAAAATAACATTTACATTAAGTCATCGAAAGGTACAGATAGGTATA  
GGAGTCTATGTGGCATTGGAAACTCACCTGATACCATGAATGGCAGCTGGTCTTCAGAG  
GGCTGTGAGCTGACATACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCTGACACA  
TTTGCAATTGATGTCCTCTGGTCCTCCATTGGTATTAAAGATTATAATATTCTTACAA  
GGATCACTCAACTAGGAATAATTATTCACTGATTGTCTTGCCATATGCATTTTACCTTC  
TGGTTCTTCAGTGAATTCAAAGCACCAAGGA

## **FIGURE 21**

GCTCCCAGCCAAGAACCTCGGGGCCGCTGCGCGGTGGGGAGGAGTTCCCCGAAACCCGGCCG  
CTAAGCGAGGCCTCCCTCCCGCAGATCCGAACGGCCTGGGCGGGGTACCCCCGGCTGGGA  
CAAGAAGCCGCCGCTGCCTGCCGGGCCCCGGGAGGGGGCTGGGCTGGGCGGGAGGCAG  
GGTGTGAGTGGGTGTGTGCGGGGGCGGAGGCTTGTGCAATCCGATAAGAAATGCTCGGG  
TGTCTTGGGCACCTACCCGTGGGGCCCGTAAGGCCTACTATATAAGGCTGCCGGCCGGAG  
CCGCCGCCGCGTCAGAGCAGGAGCGCTGCCTCAGGATCTAGGGCACGACCATCCAACCC  
GGCACTCACAGCCCCGAGCGCATCCCGTCGCCAGCCTCCGCACCCCCATGCCGG  
AGCTGCGCCGAGAGCCCCAGGGAGGTGCCATGCGGAGCGGGTGTGTGGTCCACGTATGG  
ATCCTGGCCGGCCTCTGGCTGGCGTGGCGCCGGCGCCCCCTGCCCTCTCGGACGCCGGGCC  
CCACGTGCACTACGGCTGGGCGACCCCATCCGCCTGCCACCTGTACACCTCCGGCCCC  
ACGGGCTCTCCAGCTGCTTCTGCCATCCGTGCCAGGGCGTGTGGACTGCCGCCGGGC  
CAGAGCGCCACAGTTGCTGGAGATCAAGGCAGTCGCTCTGCCACCGTGGCATCAAGGG  
CGTGCACAGCGTGCGGTACCTCTGCATGGCGCCGACGGCAAGATGCAGGGCTGCTTCAGT  
ACTCGGAGGAAGACTGTGCTTCAGAGGAGGAGATCCGCCAGATGGCTACAATGTGTACCGA  
TCCGAGAACGCCCTCCGGCTCCCTGAGCAGTGCCAAACAGCGGAGCTGTACAAGAA  
CAGAGGCTTCTTCCACTCTCTCATTCCGCCATGCTGCCCATGGTCCCAGAGGAGCCTG  
AGGACCTCAGGGGCCACTTGAATCTGACATGTTCTTCGCCCTGGAGGACCGACAGCATG  
GACCCATTGGCTTGTCAACGGACTGGAGGCCGTGAGGAGTCCCAGCTTGAGAAGTAA  
GAGACCATGCCGGCCTTCACTGCTGCCAGGGCTGTGGTACCTGCAGCGTGGGGACG  
TGCTTCTACAAGAACAGTCCCTGAGTCCACGTTCTGTTAGCTTAGGAAGAAACATCTAGAA  
GTTGTACATATTCAAGAGTTCCATTGGCAGTGCCAGTTCTAGCCAATAGACTTGTCTGAT  
CATAAACATTGTAAGCCTGTAGCTTGCCTGCCAGCTGCTGCCCTGGGCCCTATTCTGCTCCCTCGA  
GGTTGCTGGACAAGCTGCTGCACTGCTCTGAGTCTGCTGAATAACCTCCATCGATGGGAAC  
TCACCTCCTTGGAAAAATTCTTATGTCAAGCTGAAATTCTCTAATTCTCATCACTTC  
CCCAGGAGCAGCCAGAACAGCAGGAGTAGTTAATTCAAGAACAGGTGATCCACTCTGTA  
AAACAGCAGGTAATTCACTCAACCCATGTGGAATTGATCTATCTACTTCCAGGG  
ACCATTGCCCTCCCAAATCCCTCCAGGCCAGAACACTGACTGGAGCAGGCATGGCCACCAAG  
GCTTCAGGAGTAGGGGAAGCCTGGAGGCCACTCCAGGCCCTGGGACAACCTGAGAATTCCCC  
CTGAGGCCAGTTCTGTCATGGATGCTGCTGAGAATAACTGCTGTCCGGTGTACCTGC  
TTCCATCTCCAGGCCACCAGCCCTCTGCCACCTCACATGCCCTCCCATGGATTGGGGCCT  
CCCAGGCCCTGGAGGCCACTCCAGGCCCTGGGACAACCTGAGAATTCCCC  
TTGAAGACCCCAAGTCTGTCAATAACTGCTGTGAGCAGGGGGAGACCTAGAAC  
CCTTCCCCAGCACTGGTTTCAACATGATATTATGAGTAATTATTTGATATGTACA  
TCTCTTATTCTTACATTATTTATGCCCTAAATTATATTATGTATGTAAAGTGGAGTTG  
TTTGTATATTAAAGTGGAGTTGTTGT

## **FIGURE 22**

MRSGCVVVHVWILAGLWLAVAGRPLAFSDAGPHVHYGWDPIRLRHLYTSGPHGLSSCFLRI  
RADGVVDCARGQSAHSLLEIKAVALRTVAIKGVHSVRYLCMGADGKMQGLQYSEEDCAFEE  
EIRPDGYNVYRSEKHLRPLVSLSSAKQRQLYKNRGFLPLSHFLPMLPMVPEEPEDLRGHLESD  
MFSSPLETDSDMPFGLVTGLEAVRSPSFEK

**Signal peptide:**

amino acids 1-22

**Casein kinase II phosphorylation site.**

amino acids 78-82, 116-120, 190-194, 204-208

**N-myristoylation site.**

amino acids 15-21, 54-60, 66-72, 201-207

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 48-59

## **FIGURE 23**

CCCAGAAGTCAGGGCCCCGGCCTCCTGCCTGCCTGCCGCCGGACCCCTGACCTCCTCA  
GAGCAGCCGGCTGCCGCCGGAAAGATGGCGAGGAGGAGCCACCGCCTCCTGCTG  
CTGCTGCCTACCTGGTGGTCGCCCTGGCTATCATAAGGCCTATGGGTTTCTGCCAAA  
AGACCAACAAGTAGTCACAGCAGTAGAGTACCAAGAGGCTATTTAGCCTGAAAACCCAA  
AGAAGACTGTTCCAGATTAGAGTGGAAAGAAACTGGGTGGAGTGTCTCCTTGTCTAC  
TATCAACAGACTCTCAAGGTGATTTAAAAATCGAGCTGAGATGATAGATTCAATATCCG  
GATCAAAAATGTGACAAGAAGTGTGATGCCGGAAATATCGTTGTGAAGTTAGTGCCTCATCTG  
AGCAAGGCCAAACCTGGAAGAGGATAACAGTCACACTGGAAAGTATTAGTGGCTCCAGCAGTT  
CCATCATGTGAAGTACCCCTCTGCTCTGAGTGGAACTGTGGTAGAGCTACGATGTCAAGA  
CAAAGAAGGAAATCCAGCTCTGAATAACACATGGTTAAGGATGGCATCCGTTGCTAGAAA  
ATCCCAGACTGGCTCCAAAGCACCAACAGCTCATACACAATGAATAACAAAACGGAACT  
CTGCAATTAAACTGTTCCAAACTGGACACTGGAGAATATTCTGTGAAGCCCGCAATT  
TGTTGGATATCGCAGGTGTCCCTGGAAACGAATGCAAGTAGATGATCTAACATAAGTGGCA  
TCATAGCAGCCGTAGTAGTTGTGGCCTAGTGATTCCGTTGTGGCCTGGTGTATGCTAT  
GCTCAGAGGAAAGGCTACTTTCAAAAGAAACCTCCTCCAGAAGAGTAATTCTCATCTAA  
AGCCACGACAATGAGTGGAAATGTGCAGTGGCTCACGCCGTAAATCCAGCACTTGGAAAGG  
CCGGCGGGCGGATCACGAGGTAGGAGTTCTAGACCAGTCTGGCAATATGGTGAACCC  
CATCTCTACTAAAATACAAAATTAGCTGGCATGGTGGCATGTGCCTGCAGTTCCAGCTGC  
TTGGGAGACAGGAGAATCACTGAACCCGGGAGGCAGGTTGCAGTGAGCTGAGATCACGC  
CACTGCAGTCCAGCCTGGTAACAGAGCAAGATTCCATCTAAAAAATAAAATAATA  
AATAAAATACTGGTTTACCTGTAGAATTCTTACAATAATAGCTTGATATT

## **FIGURE 24**

MARRSRHRLLLLLLRLVVALGYHKAYGFSAPKDQQVVTAVEYQEAILACKTPKTVSSRLE  
WKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQNLEED  
TVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGI  
RLLENPRLGSQST  
NSSYTMNTKTGTLQFNTVSKLDTGEYSCEARN  
SVGYRRCPGKRMQVDDLNISGIIAAVVVVA  
LVI  
SVCGLGV  
CYAQRKGYFSKETSFQKS  
N  
SSKATTMSENVQWLTPV  
I  
PALW  
KAAAGGSRGQEF

**Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 130-144, 238-258

**N-glycosylation site.**

amino acids 98-102, 187-191, 236-240, 277-281

**Casein kinase II phosphorylation site.**

amino acids 39-43, 59-63, 100-104, 149-153, 205-209, 284-288

**N-myristoylation site.**

amino acids 182-188, 239-245, 255-261, 257-263, 305-311

**Amidation site.**

amino acids 226-230

## FIGURE 25

GACATCGGAGGTGGGCTAGCACTGAAACTGCTTTCAAGACGAGGAAGAGGAGGAGAAAGAG  
AAAGAAGAGGAAGATGTTGGCAACATTATTAAACATGCTCACAGCCGGACCCCTGGCAT  
CATGCTGCTATTCTGCAAATACTGAAGAAGCATGGGATTAAATATTACTCTAAATAA  
ATGAATTACTCAATCTCTATGACCATCTACATACACTCCACCTCAAAAAGTACATCAATA  
TTATATCATTAAAGGAATAGTAACCTCTCTTCAATATGCATGACATTGGACAATG  
CAATTGTGGCACTGGCACTTATTCAAGTGAAGAAAAACTTGTGGTTCTATGGCATTCA  
TTGACAAATGCAAGCATCTCCTTATCAATCAGCTCTATTGAACTTACTGCACTGACTG  
TGGAACTCTTAAGGGCCCATTACATTCTGAAGAAGAAAGCTAAGATGAAGGACATGCCACT  
CCGAATTCTATGTGCTACTTGGCCTAGCTATCACTACACTAGTACAAGCTGTAGATAAAAAG  
TGGATTGTCCACGGTTATGTACGTGTGAAATCAGGCCTGGTTACACCCAGATCCATTAT  
ATGGAAGCATCTACAGTGGATTGTAATGATTAGGTCTTTAACCTTCCCAGCCAGATTGCC  
AGCTAACACACAGATTCTCTCACAGACTAACATATTGCAAAAATTGAATACTCCACAG  
ACTTTCCAGTAAACCTTACTGGCCTGGATTATCTCAAAACAATTATCAGTCACCAAT  
ATTAATGTAAGGAAAGATGCCTCAGCTCCTTCTGTGTACCTAGAGGAAACAAACTTACTGA  
ACTGCCTGAAAATGTCGTCCGAACACTACAAGAACTCTATATTAAATCACAACT  
TGCTTCTACAATTTCACCTGGAGCCTTATTGGCCTACATAATCTTCTCGACTTCATCTC  
AATTCAAATAGATTGCAGATGATCAACAGTAAGTGGTTGATGCTCTTCAAATCTAGAGAT  
TCTGATGATTGGGAAAATCCAATTATCAGAACTCAAAGACATGAACTTTAACGCTCTTATCA  
ATCTTCGAGCCTGGTTATAGCTGGTATAAACCTCACAGAAATACAGATAACGCCCTGGTT  
GGACTGGAAAACCTAGAAAGCATCTCTTTACGATAACAGGCTTATTAAAGTACCCCATGT  
TGCTCTCAAAAGTGTAAATCTCAAATTGGATCTAAATAAAATCCTATTAAATAGAA  
TACGAAGGGGTGATTTCAGCAATATGCTACACTAAAAGAGTTGGGGATAAAATAATATGCCT  
GAGCTGATTCCATCGATAGTCTGCTGTGGATAACCTGCCAGATTTAACGAAATAGAAGC  
TACTAACACCCCTAGATTGTCTTACATTCAACCCCAATGCATTTCAGACTCCCCAAGCTGG  
AATCACTCATGCTGAACAGCAATGCTCTCAGTGCCCTGTACCATGGTACCATGGTACTCTG  
CCAAACCTCAAGGAAATCAGCATACACAGTAACCCCATCAGGTGTGACTGTGTCATCCGTG  
GATGAACATGAACAAAACCAACATTGGATTATGGAGCCAGATTCACTGTTTGCCTGGACC  
CACCTGAATTCCAAGGTCAGAATGTTGGCAAGTGCATTTCAGGGACATGATGGAAATTGT  
CTCCCTCTTATAGCTCTGAGAGCTTCTTCTAAATCTAAATGTTAGAAGCTGGGAGCTATGT  
TTCCTTCACTGTAGAGCTACTGCAGAACACCAGCCTGAAATCTACTGGATAACACCTCTG  
GTCAAAAACCTTGCCTAATACCCCTGACAGACAAGTTCTATGTCATTCTGAGGGAACACTA  
GATATAATGGCGTAACCTCCAAAGAAGGGGTTATATACTTGTATAGCAACTAACCTAGT  
TGGCGCTGACTTGAAGTCTGTTATGATCAAAGTGGATGGATCTTCCACAAGATAACAATG  
GCTCTTGAATATTAAAATAAGAGATATTCAAGGCAATTCACTGGGTGTCCTGGAAAGCA  
AGTTCTAAAATTCTCAAATCTAGTGTAAATGGACAGCCTTGTCAAGACTGAAAATTCTCA  
TGCTGCGCAAAGTGCCTGAATACCATCTGATGTCAGGTATATAATCTTACTCATCTGAATC  
CATCAACTGAGTATAAAATTGTATTGATATTCCACCATCTACAGAAAAACAGAAAAAAA  
TGTGTAATGTCACCACCAAGGTTGCACCCCTGATCAAAAAGAGTATGAAAAGAATAATAC  
CACAAACACTTATGGCCTGTCTGGAGGCCTTCTGGGATTATTGGTGTGATATGTCTTATCA  
GCTGCCCTCTCCAGAAATGAACCTGTGATGGTGGACACAGCTATGTGAGGAATTACTTACAG  
AAACCAACCTTGCATTAGGTGAGCTTATCCTCTGATAAAATCTCTGGGAAGCAGGAAA  
AGAAAAAAAGTACATCACTGAAAGTAAAGCAACTGTTAGGTTACCAACAAATATGTCCT  
AAAAACCACCAAGGAAACCTACTCCAAAAATGAAC

## **FIGURE 26**

MKDMLPLRIHVLLGLAITTLVQAVDKVDCPRLCTCEIRPWFTPRTSIYMEASTVDCNDLGLLT  
FPARLPANTQILLQTNNIAKIEYSTDFTPVNLTGLDLSQNNLSSVTNINVKKMPQLLSVYLE  
ENKLTTELPEKCLSELSNLQELYINHNLLSTISPGAFIGLHNLLRLHLNSNRLQMINSKWFDA  
LPNLEILMIGENPIIRIKDMNFKPLINLRLSLVIAGINLTEIPDNAVGLENLESISFYDNRL  
IKVPHVALQKVNLKFLLDNKNPINRIRRGDFSNMLHLKELGINNMPPELISIDSIAVDNLPD  
LRKIEATNNPRLSYIHPNAFFRLPKLESMLNSNALSALYHGTIESLPNLKEISIHSNPIRC  
DCVIRWMNMNKTNIRFMEPDSLFCVDPPFQGQNVQVHFRDMMEICLPLIAPESFPSNLNV  
EAGSYVSFHCRTAEPQPEIYWITPSGQKLLPNTLTDKFYVHSEGTLDINGVTPKEGGLYTC  
IATNLVGADLKSVMIKVDGSFPQDNNGSLNIKIRDIQANSVLVSWKASSKILKSSVKWTAFV  
KTENSHAAQSARIPSDVKVYNLTHLPSTEYKICIDIPTIYQKNRKKCVNVTTKGLHPDQKE  
YEKNNTTLLMACLGGLLGIIGVICLISCLSPEMNCGGHSYVRNYLQKPTFALGELYPPLIN  
LWEAGKEKSTSLKVKATVIGLPTNMS

**Signal sequence:**

amino acids 1-22

**Transmembrane domain:**

amino acids 633-650

**N-glycosylation site.**

amino acids 93-97, 103-107, 223-227, 382-386, 522-526, 579-583,  
608-612, 624-628, 625-629

**Casein kinase II phosphorylation site.**

amino acids 51-55, 95-99, 242-246, 468-472, 487-491

**Tyrosine kinase phosphorylation site.**

amino acids 570-579

**N-myristoylation site.**

amino acids 13-19, 96-102, 158-164, 221-227, 352-358, 437-443,  
491-497, 492-498, 634-640, 702-708

**Cell attachment sequence.**

amino acids 277-280

## **FIGURE 27**

CCCCGGGACTGGCGCAAGGTGCCAAGCAAGGAAAGAAATAATGAAGAGACACATGTGTTAG  
CTGCAGCCTTTGAAACACGCAAGAAGGAAATCAATAGTGTGGACAGGGCTGGAACCTTAC  
CACGCTTGTGGAGTAGATGAGGAATGGCTCGTATTATGCTGACATTCCAGCATGAATCT  
GGTAGACCTGTGGTTAACCGTTCCCTCCATGTGTCTCCTCCTACAAAGTTGTTCTTA  
TGATACTGTGCTTCATTCTGCCAGTATGTGTCCCAAGGGCTGTCTTGTCTCCTCTGGG  
GGTTAAATGTCACCTGTAGCAATGCAAATCTCAAGGAAATACCTAGAGATCTTCCTCCTGA  
AACAGTCTTACTGTATCTGGACTCCAATCAGATCACATCTATTCCAATGAAATTAAAGG  
ACCTCCATCAACTGAGAGTTCTAACCTGTCCAAAATGGCATTGAGTTATCGATGAGCAT  
GCCTCAAAGGAGTAGCTGAAACCTTGCAGACTCTGGACTTGTCCGACAATCGGATTCAAAG  
TGTGCACAAAATGCCTCAATAACCTGAAGGCCAGGCCAGAATTGCCAACACCCTGGC  
ACTGCGACTGTACTCTACAGCAAGTTCTGAGGAGCATGGCGTCCAATCATGAGACAGCCCAC  
AACGTGATCTGTAAAACGTCCGTGTTGGATGAACATGCTGGCAGACCATTCTCAATGCTGC  
CAACGACGCTGACCTTGTAAACCTCCCTAAAAAAACTACCGATTATGCCATGCTGGTCACCA  
TGTTGGCTGGTTCACTATGGTGTCTCATATGTGGTATTATGTGAGGCAAAATCAGGAG  
GATGCCGGAGACACCTCGAATACTTGAAATCCCTGCCAAGCAGGCAGAAGAAAGCAGATGA  
ACCTGATGATATTAGCACTGTGGTAAGTGTCCAAACTGACTGTCAATTGAGAAAGAAAGAAA  
GTAGTTGCATTGCAGTAGAAATAAGTGGTTACTTCTCCATCCATTGTAAACACATTGAA  
ACTTGTATTCAGTTTTGAATTATGCCACTGCTGAACCTTAACAAACACTACAACA  
TAAATAATTGAGTTAGGTGATCCACCCCTTAATTGTACCCCCGATGGTATATTCTGAGT  
AAGCTACTATCTGAACATTAGTTAGATCCATCTCACTATTAAATAATGAAATTATTTTTT  
AATTAAAAGCAAATAAGCTTAACTTGAACCAGGGAAAAAAAAAAAAAAACA

## **FIGURE 28**

MNLVDLWLTRSLSMCLLLQSFVLMILCFHSASMC PKGCLCSSGGLNVTC SNANLKEIPRDL  
PPETVLLYLDSNQITSIPNEIFKDLHQLRVLNLSKNGIEFIDEHAFKGVAETLQTLDSL DNR  
IQSVHKNAFNNLKARARIANNPWHCDCTLQQVLRSMASNHETAHNVICKTSVLDEHAGRPFL  
NAANDADLCNLPKKTTDYAMLVTMFGWFTMVISYVVYYVRQNQEDARRHLEYLKSLPSRQKK  
ADEPDDISTVV

**Signal sequence:**

amino acids 1-33

**Transmembrane domain:**

amino acids 205-220

**N-glycosylation site.**

amino acids 47-51, 94-98

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 199-203

**Casein kinase II phosphorylation site.**

amino acids 162-166, 175-179

**N-myristoylation site.**

amino acids 37-43, 45-51, 110-116

## **FIGURE 29**

## **FIGURE 30**

MQVSKRMLAGGVRSMPSPLLACWQPILLVLGSVLSGSATGCPPRCECSAQDRAVLCHRKCF  
VAVPEGIPTETRLLDLGKNRIKTLNQDEFASFPHLEELELNENIVSAVEPGAFNNLFNLRTL  
GLRSNRLKLIPLGVFTGLSNLTQDISENKIVILLDYMFDLYNLKSLEVGDNDLVYISHRA  
FSGLNSLEQLTLEKCNLTSIPTEALSHLHGLIVLRLRHLNINAIRDYSFKRLYRLKVLEISH  
WPYLDTMTPNCLYGLNLTSLSITHCNLTAVPYLAVRHLVYLRFLNLSYNPISTIEGSMLHEL  
LRLQEIQLVGGQLAVVEPYAFRGLNYLRLVNVSGNQLTLEESVFHSVGNLETLILDSNPLA  
CDCRLLWVFRWRRLNFNRQQPTCATPEFVQGKEFKDFPDVLLPNYFTCRRARIRDRKAQQV  
FVDEGHTVQFVCRADGDPPIALWLSPRKHLVSAKSNGRLTVFDGTLEVRYAQVQDNGTYL  
CIAANAGGNDSMPAHLHVRSYSPDWPHQPNKTFAFISNQPGEGEANSTRATVPFPFDIKTLI  
IATTMGFISFLGVVLFCLVLLFLWSRGKGNTKHNIEIEYVPRKSDAGISSADAPRKFNMKMI

**Signal sequence:**

amino acids 1-41

**Transmembrane domain:**

amino acids 556-578

**N-glycosylation site.**

amino acids 144-148, 202-206, 264-268, 274-278, 293-297, 341-345,  
492-496, 505-509, 526-530, 542-546

**Casein kinase II phosphorylation site.**

amino acids 49-53, 108-112, 146-150, 300-304, 348-352, 349-353,  
607-611

**Tyrosine kinase phosphorylation site.**

amino acids 590-598

**N-myristoylation site.**

amino acids 10-16, 32-38, 37-43, 113-119, 125-131, 137-143,  
262-268, 320-326, 344-350, 359-365, 493-499, 503-509, 605-611

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 32-43

## FIGURE 31

CCACCGCGTCCGCACCTCGGCCCCGGGCTCCGAAGCGGCTCGGGGCGCCCTTCGGTCAAC  
ATCGTAGTCCACCCCTCCCCATCCCCAGCCCCGGGATTCAAGGCTGCCAGCGCCAGCC  
AGGGAGCCGGCCGGGAAGCGCGATGGGGGCCCCAGCCGCTCGCTCCTGCTCCTGCTCCTGC  
TGTTCGCCTGCTGCTGGCGCCGGGGCAACCTCTCCCAGGACGACAGCCAGCCCTGG  
ACATCTGATGAAACAGTGGTGGCTGGCACC GTGGT GCTCAAGT GCCAAGT GAAAG ATCA  
CGAGGACTCATCCCTGCAATGGCTAACCTGCTCAGCAGACTCTACTTTGGGAGAAGA  
GAGCCCTCGAGATAATCGAATTCACTGGTTACCTCACGCCAACGAGCTCAGCATCAGC  
ATCAGCAATGTGGCCCTGGCAGACGAGGGCGAGTACACCTGCTCAATCTCACTATGCCCTGT  
GCGAACTGCCAAGTCCCTCGTCACTGTGCTAGGAATTCCACAGAACGCCATCATCACTGGTT  
ATAAACTTCATTACGGGAAAAAGACACAGCCACCCCTAAACTGTCAGTCTTCTGGGAGCAAG  
CCTGCAGCCGGCTCACCTGGAGAAAGGGTACCAAGAACACTCCACGGAGAACCAACCGCAT  
ACAGGAAGATCCCAATGGTAAAACCTTCACTGTCAGCAGCTCGGTGACATTCCAGGTTACCC  
GGGAGGATGATGGGCGAGCATCGTGTGCTGTGAACCATGAATCTCTAAAGGGAGCTGAC  
AGATCCACCTCTCAACGCATTGAAGTTTATACACACCAACTGCGATGATTAGGCCAGACCC  
TCCCCATCCTCGTGAGGGCCAGAACGCTGTTGCTACACTGTGAGGGTCGCGGAATCCAGTCC  
CCCAGCAGTACCTATGGGAGAAGGAGGGCAGTGTGCCACCCCTGAAGATGACCCAGGAGAGT  
GCCCTGATCTTCCCTTCCTCAACAAGAGTACAGTGGCACCTACGGCTGCACAGCCACCA  
AACATGGGCAGCTACAAGGCCTACTACACCCCTCAATGTTAATGACCCAGTCCGGTGCCT  
CCTCCTCCAGCACCTACCACGCCATCATCGGTGGATCGTGGCTTCATTGTCTCCTGCTG  
CTCATCATGCTCATCTCCTGGCCACTACTTGATCCGGCACAAAGGAACCTACCTGACACA  
TGAGGCAAAAGGCTCCGACGATGCTCCAGACGCGGACACGCCATCATCAATGCAGAAGGGC  
GGCAGTCAGGAGGGACGACAAGAAGGAATATTCACTTAGAGGCGCTGCCACTTCTGC  
GCCCCCCAGGGGCCCTGTGGGACTGCTGGGCCGTACCAACCGGACTTGTACAGAGCAA  
CCGCAGGGCCGCCCTCCGCTTGCTCCCCAGCCCACCCACCCCTGTACAGAATGTCTGC  
TTTGGGTGCGGTTTGTACTCGGTTGGAATGGGAGGGAGGAGGGCGGGGGAGGGAGGG  
TTGCCCTCAGCCCTTCCGTGGCTCTGCATTGGTTATTATTATTGTAAACAATCC  
CAAATCAAATCTGTCTCCAGGCTGGAGAGGCAGGAGCCCTGGGGTGAGAAAAGCAAAAAACA  
AACAAAAAACAA

## **FIGURE 32**

MGAPAASLLLLLFAACCWAPGGANLSQDDSQWPWTSDETVVAGGTVVLKCQVKDHEDSSLQW  
SNPAQQTLYFGEKRALRDNRQLVTSTPHELYSISISNVALADEGEYTCISIFTMPVRTAKSLV  
TVLGIHQKPIITGYKSSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGK  
TFTVSSSVTFQVTREDDGASIVCSVNHESLKGADRSTSQRIEVLYTPTAMIRPDPPHPREGQ  
KLLLHCEGRGNPVPQQYLWEKEGSVPPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSYKA  
YYTILNVNDPSPVPSSSSTYHAIIGGIVAFIVFLLLIMLIFLGHYLIRHKGTYLTHEAKGSDD  
APDADTAIINAEGGQSGGDDKKEYFI

**Signal sequence:**

amino acids 1-20

**Transmembrane domain:**

amino acids 331-352

**N-glycosylation site.**

amino acids 25-29, 290-294

**Casein kinase II phosphorylation site.**

amino acids 27-31, 35-39, 89-93, 141-145, 199-203, 388-392

**N-myristoylation site.**

amino acids 2-8, 23-29, 156-162, 218-224, 295-301, 298-304,  
306-310, 334-340, 360-364, 385-389, 386-390

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 7-18

## FIGURE 33

GGGGGTTAGGGAGGAAGGAATCCACCCCCACCCCCCAAACCCCTTTCTCCTTCTGG  
CTCGGACATTGGAGCACTAAATGAACCTGAATTGTGCTGTGGCGAGCAGGATGGTCGCTG  
TTACTTTGTGATGAGATCGGGGATGAATTGCTCGCTTAAAAATGCTGCTTGGATTCTGTT  
GCTGGAGACGTCTTTGCCGCTGGAAACGTTACAGGGGACGTTGCAAAGAGAAGA  
TCTGTTCTGCAATGAGATAGAAGGGACCTACACGTAGACTGTGAAAAAAAGGGCTTCACA  
AGTCAGCGCTTCACTGCCCGACTTCCCAGTTTACCAATTATTCATGGCAATT  
CCTCACTCGACTTTCCCTAATGAGTCGCTAACATTATAATGCGGTTAGTTGCACATGG  
AAAACAATGGCTTGCATGAAATCGTCCGGGGCTTTCTGGGGCTGCAGCTGGTAAAAGG  
CTGCACATCAACAACAAGATCAAGTCTTTCGAAAGCAGACTTTCTGGGGCTGGACGA  
TCTGGAATATCTCCAGGCTGATTTAATTATTACGAGATATAAGACCCGGGGCTTCCAGG  
ACTTGAACAAGCTGGAGGTGCTCATTAAATGACAATCTCATCAGCACCCACTGCCAAC  
GTGTTCCAGTATGTGCCCATACCCACCTCGACCTCCGGGTAACAGGCTGAAAAGCTGCC  
CTATGAGGAGGTCTGGAGCAAATCCCTGGTATTGCGGAGATCCTGCTAGAGGATAACCC  
GGGACTGCACCTGTGATCTGCTCTCCCTGAAAGAATGGCTGGAAAACATTCCAAGAATGCC  
CTGATCGGCCAGTGGTCTCGAAGCCCCACCACTGCAGGGTAAAGACCTCAATGAAAC  
CACCGAACAGGACTTGTGCTTTGAAAAACCGAGTGGATTCTAGTCTCCGGCCCGCCCTG  
CCCAAGAACAGGACCTTGCTCCCTGGACCCCTGCCACTCCTCAAGACAAATGGCAAGAG  
GATCATGCCAACACCAGGTCTGCTCAAACGGAGGTACAAAGATCCCAGGCAACTGGCAGAT  
CAAATCAGACCCACAGCAGCGATAGCGACGGTAGCTCAGGAACAAACCCCTAGCTAAC  
GTTTACCTGCCCTGGGGCTGCAGCTGCGACCACATCCCAGGGTGGGTTAAAGATGAAC  
TGCAACAAACAGGAACGTGAGCAGCTTGCTGATTGAAGCCCAAGCTCTAACGTGCAGGA  
GCTTTCTACGAGATAACAAGATCCACAGCATCCGAAAATCGCACTTGTGGATTACAAGA  
ACCTCATTCTGTTGGATCTGGCAACAAATAACATCGCTACTGTAGAGAACAAACACTTCAAG  
AACCTTTGGACCTCAGGTGGCTATACATGGATAGCAATTACCTGGACACGCTGTCCGGGA  
GAAATTGCGGGGCTGCAAAACCTAGAGTACCTGAACAGTGGAGTACAACGCTATCCAGCTCA  
TCCTCCGGCACTTCAATGCCATGCCAAACTGAGGATCCTCATTCTCAACAAACACCTG  
CTGAGGTCCCTGCCTGTGGACGTGTCGCTGGGTCTCGCTCTAAACTCAGCCTGCACAA  
CAATTACTCATGTACCTCCGGTGGCAGGGGTGCTGGACCAGTTAACCTCCATCATCCAGA  
TAGACCTCCACGAAACCCCTGGGAGTGCTCCTGCACAATTGTGCCTTCAAGCAGTGGGCA  
GAACGCTTGGGTTCCGAAGTGCTGATGAGCGACCTCAAGTGTGAGACGCCGGTGAACCTT  
TAGAAAGGATTTCATGCTCTCTCCAATGACGAGATCTGCCCTAGCTGTACGCTAGGATCT  
CGCCCACGTTAACCGCACAGTAAAACAGCACTGGGTTGGCGAGACCGGGACGCACCTCC  
AACTCCTACCTAGACACCAGCAGGGTGTCCATCTGGTGTGGCTCCGGACTGCTGCTGGT  
GTTTGTACCTCCGCCTTCACCGTGGGGCATGCTCGTGTATTCTGAGGAACCGAAAGC  
GGTCCAAGAGACGAGATGCCAACTCCTCCCGTCCGAGATTAACTCCCTACAGACAGTCTGT  
GAECTTCTACTGGCACAATGGGCTTACAACGAGATGGGGCCACAGAGTGTATGACTG  
TGGCTCTACTCGCTCTCAGACTAAAGACCCCAACCCAAATAGGGGAGGGCAGAGGGAAAGGCG  
ATACATCCTCCCCACCGCAGGCACCCGGGGCTGGAGGGCGTGTACCCAAATCCCCGCG  
CCATCAGCCTGGATGGCATAAGTAGATAAAACTGTGAGCTCGCACAAACGAAAGGGCT  
GACCCCTTACTTAGCTCCCTCTTGAAACAAAGAGCAGACTGTGGAGAGCTGGAGAGCGCA  
GCCAGCTCGCTTTGCTGAGAGGCCCTTTGACAGAAAGGCCAGCACGACCCCTGCTGGAAG  
AACTGACAGTGCCCTGCCCTGGCCCCGGGGCTGTGGGTTGGATGCCCGGGTTCTATAC  
ATATATACATATATCCACATCTATATAGAGAGATAGATATCTATTTCCCTGTGGATTAG  
CCCCGTGATGGCTCCCTGTTGGCTACGCAGGGATGGCAGTTGCACGAAGGCATGAATGTAT  
TGTAAATAAGTAACTTGACTCTGAC

## **FIGURE 34**

MLLWILLLETSLCFAAGNVTGVCCKICSCNEIEGDLHVDCEKKGFTSLQRFTAPTSQFYH  
LFLHGNSLTRLFPNEFANFYNAVSLHMENNGLHEIVPGAFGLQLVKRLHINNNKIKSFRKQ  
TFLGLDDLEYLQADFNLLRIDPGAFQDLNKEVLILNDNLISTLPANVFQYVPITHLDLRG  
NRLKTLPYEEVLEQIPGIAEILLEDPWDCTCDLLSLKEWLENIPKNALIGRVVCEAPTRLQ  
GKDLNETTEQDLCPLKNRVDSSLPPAQAEEFTAPGPLPTPKTNGQEDHATPGSAPNGGTK  
IPGNWQIKIRPTAAIATGSSRNKPLANSLPCPGCSDHIPGSGLKMNCNNRNVSSLADLKP  
KLSNVQELFLRDNKIHSIRKSHFVDYKNLILLLDGNNNIATVENNTFKNLLDLRWLYMDSNY  
LDTLSREKFAGLQNLEYLNVEYNIAIQILILPGTFNAMPKLRILILNNNLLRSLPVDVFAGVSL  
SKLSLHNMYFMYLPVAGVLDQLTSIIQIDLHGNPWECSCTIVPFKQWAERLGSEVLMSDLKC  
ETPVNFFRKDFMLLSNDEICPQLYARISPTLTSHSKNSTGLAETGTHNSYLDTSRVSISVL  
VPGLLLVFVTSAAFTVVGMLVFILRNRKRSKRRDANSASEINSLQTVCDSSYWHNGPYNADG  
AHRVYDCGSHSLSD

**Signal sequence:**

amino acids 1-15

**Transmembrane domain:**

amino acids 618-638

**N-glycosylation site.**

amino acids 18-22, 253-257, 363-367, 416-420, 595-599, 655-659

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 122-126, 646-650

**Casein kinase II phosphorylation site.**

amino acids 30-34, 180-184, 222-226, 256-260, 366-370, 573-577,  
608-612, 657-661, 666-670, 693-697

**N-myristoylation site.**

amino acids 17-23, 67-73, 100-106, 302-308, 328-334, 343-349,  
354-360, 465-471, 493-499, 598-604, 603-609

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 337-348

## FIGURE 35

AGTCGACTGCGTCCCTGTACCCGGGCCAGCTGTGTTCTGACCCCCAGAATAACTCAGGGC  
TGCACCGGGCTGGCAGCGCTCCGCACACATTCTGTGCGGGCTAAGGGAAACTGTTGGC  
CGCTGGGCCCGCGGGGGATTCTTGGCAGTTGGGGGTCCGTGGGAGCGAGGGCGGAGGGG  
AAGGGAGGGGGAACCGGGTTGGGAAGCCAGCTGTAGAGGGCGGTGACCGCGCTCCAGACAC  
AGCTCTGCGTCCTCGAGCGGGACAGATCCAAGTTGGGAGCAGCTCTGCGTGCCTGGGGCCTCAG  
**AGAATGAGGCCGGCTTCGCCCTGTGCCCTCTGGCAGGCGCTCTGGCCCGGGCCGGCG**  
CGCGAACACCCCCACTGCGGACCGTGTGGCTCGCTCGGCCCTGGGGCCTGCTACAGCCTGC  
ACCAAGCTACCATGAAGCGGCAGGGCGAGGAGGCTGCATCCTGCGAGGTGGGGCGCTC  
AGCACCGTGCCTGCAGCTCGCGCTGTGCTCGCGCTCTGCGGGCAGGCCAGG  
GCCCGGAGGGGGCTCAAAGACCTGCTGTTCTGGTCCGACTGGAGCGCAGGCCAGG  
GCACCCCTGGAGAACGAGCCTTGCAGGGTTCTCTGGCTGTCTCCGACCCGGCGGTCTC  
GAAAGCGACACGCTGCAGTGGGTGGAGGAGCCCCAACGCTCCTGCACCGCGGGAGATGCGC  
GGTACTCCAGGCCACCGTGGGTGAGGCCGAGGCTGGAAAGGAGATGCGATGCCACCTGC  
GCGCCAACGGCTACCTGTGCAAGTACCAAGTTGAGGTCTTGTGCTCTGCGCCGCCGG  
GCCGCTCTAACTTGAGCTATCGCGCCCTTCCAGCTGCACAGCGCCGCTCTGGACTTCAG  
TCCACCTGGGACCGAGGTGAGTGCCTCTGCCGGGACAGCTCCGATCTCAGTTACTTGCA  
TCGCGGACGAAATCGCGCTCGCTGGACAAACTCTCGGGCGATGTGTTGTCCCTGCC  
GGGAGGTACCTCCGTGCTGGCAAATGCGCAGAGCTCCCTAAGTGCCTAGACGACTTGGAGG  
CTTGCCTGCGAATGTGCTACGGCTTGCAGCTGGGAAGGACGGCGCTTGTGACCA  
GTGGGGAGGACAGCCGACCCCTGGGGGACGGGGTGCCACCAGGCGCCGCCACT  
GCAACCAGCCCCGTGCCGCAGAGAACATGGCAAATCAGGGTCGACGAGAACGACTTGGAG  
ACCAACTGTCCCTGAACAAGACAATTCAAGTAACTATCTATTCTGAGATTCTCGATGGGAT  
CACAGAGCACGATGTTACCCCTCAAATGTCCCTCAAGCCGAGTCAGGCCACTATCACC  
CCATCAGGGAGCGTGATTTCAAGTTAATTCTACGACTCCTCTGCCACTCCTCAGGCTT  
CGACTCCTCCTCTGCCGTGGTCTTCATATTGTGAGCACAGCAGTAGTAGTGTGTTGGT  
TGACCATGACAGTACTGGGCTTGTCAAGCTCTGCTTACGAAAGCCCTTCCAGCCA  
AGGAAGGAGTCTATGGGCCCGGGCTGGAGAGTGATCCTGAGCCGCTGCTTGGCTC  
CAGTTCTGCACATTGCACAAACATGGGTGAAAGTCGGGACTGTGATCTGCCAGAG  
CAGAGGGTGCCTTGCAGGGAGTCCCTTGGCTCTAGTGTGCA**AGGAAACAGGGGA**  
CATGGGCACTCCTGTGAACAGTTTCACTTTGATGAAACGGGAACCAAGAGGAACCTAC  
TTGTGTAAGTACAATTCTGCAGAAATCCCCCTCCTCTAAATTCCCTTACTCCACTGAG  
GAGCTAAATCAGAACACTGCACACTCCTCCCTGATGATAGAGGAAGTGGAAAGTGCCTT  
TGGTGTGATACTGGGGACCGGGTAGTGTGCTGGGAGAGATATTCTTATGTTATTGGAGA  
TTTGGAGAAGTGAATTGAACTTTCAAGACATTGGAAACAAATAGAACACAATATAATTACA  
TTAAAAAATAATTCTACCAAAATGGAAAGGAAATGTTCTATGTTGTCAGGCTAGGAGTAT  
ATTGGTTGAAATCCCAGGGAAAAAATAAAAATTAAAGGATTGTTGAT

## **FIGURE 36**

MRPAFALCLLWQALWPGPGGGEHPTADRAGCSASGACYSLHHATMKRQAAEEACILRGGALS  
TVRAGAELRAVLALLRAGPGPGGGSKLLLFWVALERRSHCTLENEPLRGFSWLSSDPGGLE  
SDTLQWVEEPQRSCTARRCAVLQATGGVEPAGWKEMRCHLRANGYLCKYQFEVLCAPRPGA  
ASNLSYRAPFQLHSAALDFSPPGTEVSALCRGQLPISVTCIADEIGARWDKLSGDVLCPCPG  
RYLRAGKCAELPNCLDDLGGFACECATGFELGKDGRSCVTSGEQPTLGGTGVPTRRPPATA  
TSPVPQRTWPIRVDEKLGETPLVPEQDNSVTSIPEIPRWGSQSTMSTLQMSLQAESKATITP  
SGSVISKFNSTTSSATPQAFDSSSAVVFIFVSTAVVVLVILMTVLGLVKLCFHESPSSQPR  
KESMGPPGLESDEPAALGSSAHCTNNGVKVGDCDLRDRAEGALLAESPLGSSDA

**Signal sequence:**

amino acids 1-16

**Transmembrane domain:**

amino acids 399-418

**N-glycosylation site.**

amino acids 189-193, 381-385

**Glycosaminoglycan attachment site.**

amino acids 289-293

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 98-102, 434-438

**Casein kinase II phosphorylation site.**

amino acids 275-279, 288-292, 342-346, 445-449

**N-myristoylation site.**

amino acids 30-36, 35-41, 58-64, 59-65, 121-127, 151-157,  
185-191, 209-215, 267-273, 350-356, 374-380, 453-459, 463-469,  
477-483

**Aspartic acid and asparagine hydroxylation site.**

amino acids 262-274

## FIGURE 37

CGGACGGCTGGGATTCAAGCAGTGGCTGTGGCTGCCAGAGCAGCTCCTCAGGGGAAACTAAG  
CGTCGAGTCAGACGGCACCATAATCGCCTTAAAGTGCCTCCGCCCTGCCGGCGCGTATC  
CCCCGGCTACCTGGGCCCGCCCGCGCGGTGCGCGCGTGAAGAGGGAGCGCGCGGGCAGCCGA  
GCGCCGGTGTGAGCCAGCGCTGCTGCCAGTGTGAGCGCGGTGTGAGCGCGGTGGGTGCGGA  
GGGGCGTGTGCGCGCGCGCGCGTGGGTGCAAACCCCGAGCGTCTACGCTGCC**ATGA**  
GGGGCGCGAACGCCTGGCGCCACTCTGCCTGCTGGCTGCCGCCACCCAGCTCTGCCGG  
CAGCAGTCCCCAGAGAGACCTGTTTACATGTGGTGGCATTCTTACTGGAGAGTCTGGATT  
TATTGGCAGTGAAGGTTCTGGAGTGTACCCCTCAAATAGCAAATGTACTTGGAAAATCA  
CAGTTCCCAGAAGGAAAAGTAGTCGTTCTCAATTCCGATTCAAGACCTCGAGAGTGACAAC  
CTGTGCCGCTATGACTTGTGGATGTGTACAATGGCCATGCCAATGCCAGCGCATTGGCCG  
CTTCTGTGGCACTTCCGGCTGGAGGCCCTGTGTCCAGTGGCAACAAGATGATGGTGCAGA  
TGATTCTGATGCCAACACAGCTGGCAATGGCTCATGCCATGTTCTCGCTGCTGAACCA  
AACGAAAGAGGGATCAGTATTGTGGAGGACTCCTGACAGACCTCCGGCTTTAAAAC  
CCCCAACTGCCAGACCGGGATTACCTGCAGGAGTCACTTGTGTGTGGCACATTGTAGCCC  
CAAAGAATCAGTTATAGAATTAAAGTTGAGAAGTTGATGTGGAGCGAGATAACTACTGC  
CGATATGATTATGTGGCTGTGTTAATGGCGGGAAAGTCAACGATGCTAGAAGAATTGGAAA  
GTATTGTGGTGATAGTCCACCTGCGCCAATTGTGTCTGAGAGAAATGAACCTTATTCACT  
TTTATCAGACTTAAGTTAATGCAGATGGGTTATTGGTCACTACATATTCAAGGCCAAA  
AAACTGCCTACAACACTACAGAACAGCCTGTCACCACATTCCCTGTAACCACGGGTTAAA  
ACCCACCGTGGCCTGTGTCACAAAAGTAGACGGACGGGACTCTGGAGGGCAATTATT  
GTTCAAGTGACTTTGATTAGCCGGCACTGTTATCACAACCATCACTCGCGATGGAGTTG  
CACGCCACAGTCTCGATCATCACATCTACAAAGAGGAAATTGGCATTAGCAGGCAGGG  
CAAGAACATGAGTGCCAGGCTGACTGTCGTGCAAGCAGTGCCTCTCAGAACAGAGTC  
TAAATTACATTATTATGGGCAAGTAGGTGAAGATGGCGAGGAAAATCATGCCAACAGC  
TTTATCATGATGTTCAAGACCAAGAACATCAGAACGCTCCTGGATGCCCTAAAAAATAAGCAATG  
**TTAACAGTGA**ACTGTGTCATTAAAGCTGTATTCTGCCATTGCCCTTGAAGATCTATGTC  
TCTCAGTAGAAAAAAATACTTATAAAATTACATATTCTGAAAGAGGATTCCGAAAGATGG  
GAAGTGGTGACTCTCACATGATGGAGGTATGAGGCCCTCCGAGATAGCTGAGGGAAAGTTCTT  
TGCCTGCTGTCAGAGGAGCAGCTATGATTGAAACCTGCCACTTAGTGCAGGTAGAGGA  
AGCTAAAAGTGTCAAGCGTTGACAGCTTGGAAAGCGTTATTTATACATCTGTAAAAGGAT  
ATTTAGAATTGAGTTGTGTGAAGATGTCAAAAAAAGATTTAGAAGTGCATATTATAGT  
GTTATTGTTTCACCTCAAGCCTTGCCTGAGGTGTTACAATCTGCTTGCCTTCTA  
AATCAATGCTTAATAAAATTAAAGGAAAAAA

## **FIGURE 38**

MRGANAWAPLCLLLAAATQLSRQQSPERPVFTCGGILTGESFIGSEGFPGVYPPNSKCTWK  
ITVPEGKVVVLNFRFIDLESNDLCRYDFVDVYNGHANGQRIGRFCGTFRPGALVSSGNKMMV  
QMISDANTAGNGFMAMFSAAEPNERGQYCGGLLDRPSGSFKTPNWPDRDYPAGVTCVWHIV  
APKNQLIELKFEKFDVERDNYCRYDYVAVFNGGEVNDARRIGKYCGDSPPAPIVSERNELLI  
QFLSDLSLTADGFIGHYIFRPKKLPTTTEQPVTTFPVTTGLKPTVALCQQKCRTGTLEGN  
YCSSDFVLAGTVITTITRD GSLHATVSIINIYKEGNLAIQQAGKNMSARLTVVCKQCPLLRR  
GLNYIIMGQVGEDGRGKIMPNSFIMMFKTKNQKLLDALKNKQC

**Signal sequence:**

amino acids 1-23

**N-glycosylation site.**

amino acids 355-359

**Casein kinase II phosphorylation site.**

amino acids 64-68, 142-146, 274-278

**Tyrosine kinase phosphorylation site.**

amino acids 199-208

**N-myristoylation site.**

amino acids 34-40, 35-41, 100-106, 113-119, 218-224, 289-295,  
305-311, 309-315, 320-326, 330-336

**Cell attachment sequence.**

amino acids 149-152

## **FIGURE 39**

CGGACGCGTGGCGGACGCGTGGCGGCCACGGGCCCGGGCTGGGCGGTGCTTCTT  
CCTTCTCCGTGGCCTACGAGGGTCCCCAGCCTGGTAAAGATGGCCCCATGGCCCCGAAGG  
GCCTAGTCCCAGCTGTGCTCTGGGCCTCAGCCTCTCCTCAACCTCCCAGGACCTATCTGG  
CTCCAGCCCTCTCCACCTCCCCAGTCTCTCCCCGCCTCAGCCCCATCCGTGTACATACCTG  
CCGGGGACTGGTTGACAGCTTAACAAGGGCTGGAGAGAACCATCCGGACAACCTTGGAG  
GTGGAAACACTGCCTGGAGGAAGAGAATTGTCAAATACAAAGACAGTGAGACCCGCCTG  
GTAGAGGTGCTGGAGGGTGTGCAGCAAGTCAGACTCGAGTGCCACCGCCTGCTGGAGCT  
GAGTGAGGAGCTGGTGGAGAGCTGGTGGTTACAAGCAGCAGGAGGCCGGACCTCTTCC  
AGTGGCTGTGCTCAGATTCCCTGAAGCTCTGCTGCCCGCAGGCACCTCGGGCCCTCCTGC  
CTTCCCTGTCTGGGGAACAGAGAGGCCCTGGGTGGCTACGGCAGTGTGAAGGGAGAAGG  
GACACGAGGGGGCAGCGGCACTGTGACTGCCAAGCCGGCTACGGGGTGAGGCCTGTGGCC  
AGTGTGGCCTGGCTACTTGAGGCAGAACGCAACGCCAGCCATCTGGTATGTTGGCTTGT  
TTTGGCCCTGTGCCGATGCTCAGGACCTGAGGAATCAAACGTGTTGCAATGCAAGAAGGG  
CTGGGCCCTGCATCACCTCAAGTGTGAGACATTGATGAGTGTGGCACAGAGGGAGCCA  
GTGGAGCTGACCAATTCTGCGTGAACACTGAGGGCTCCTATGAGTGCCGAGACTGTGCCAAG  
GCCTGCCTAGGCTGCATGGGGCAGGCCAGGTGCTGTAAGAAGTGTAGCCCTGGCTATCA  
GCAGGTGGCTCCAAGTGTCTCGATGTGGATGAGTGTGAGACAGAGGTGTCCGGAGAGA  
ACAAGCAGTGTGAAAACACCGAGGGCGTTATCGCTGCATCTGTGCCGAGGGCTACAAGCAG  
ATGGAAGGCATCTGTGTGAAGGAGCAGATCCAGAGTCAGCAGGCTTCTCAGAGATGAC  
AGAAGACGAGTTGGTGGTGTGCAGCAGATGTTCTTGGCATCATCTGTGCACTGGCCA  
CGCTGGCTGCTAAGGGCAGTTGGTGTACCGCCATCTCATTGGGCTGTGGCGGCCATG  
ACTGGCTACTGGTGTCAAGAGCAGTGACCGTGTGGAGGGCTTCATCAAGGGCAGATA  
ATCGCGGCCACCACCTGTAGGACCTCCTCCCACCCACGCTGCCCGAGAGCTTGGCTGCC  
TCCTGCTGGACACTCAGGACAGCTTGGTTATTTGAGAGTGGGTAAGCACCCCTACCTG  
CCTTACAGAGCAGCCCAGGTACCCAGGCCGGCAGACAAGGCCCTGGGTAAAAAGTAGC  
CCTGAAGGTGGATACCATGAGCTCTCACCTGGCGGGACTGGCAGGCTTCACAATGTGTGA  
ATTTCAAAAGTTTCTTAATGGTGGCTGCTAGAGCTTGGCCCTGCTTAGGATTAGGTG  
GTCCTCACAGGGTGGGCCATCACAGCTCCCTGAGCTGCTGCCAGCTGCTGCCAGTTCTGT  
TCTGTGTTCACACATCCCCACACCCATTGCCACTTATTATTCATCTCAGGAAATAAGA  
AAGGTCTGGAAAGTTAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 40**

MAPWPKGLVPAVLWGLSLFLNLPGPPIWLQPSPPPQSSPPPQPHPCHTCRGLVDSFNKGLERTIRDNFGGGNTAWEENLSKYKDSETRLVEVLEGVCSKSDFECHRLLELSEELVESWWFHKQQEAPDLFQWLCSDSLKCCPAGTFGPSCLPCCPGTERPCGGYQCEGEGTRGGSGHCDCQAGYGGEACGQCGLGYFEAERNASHLVC SACFGPCARCSGPPEESNCLQCKKGWALHHLKCVDIDE CGTEGANCADQFCVNTEGSYECRDCAKACLGCMGAGPGRCKKCSPGYQQVGSKCLDVDECE TEVCPGENKQCENTEGGYRCICAEGYKQMEGICVKEQI PESAGFFSEMTEDELVVLQQMFFG IIICALATLAAGDLVFTAIFIGAVAAMTGYWLSERSDRVLEGF IKGR

**Signal sequence:**

amino acids 1-29

**Transmembrane domain:**

amino acids 372-395

**N-glycosylation site.**

amino acids 79-83, 205-209

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 290-294

**Casein kinase II phosphorylation site.**

amino acids 63-67, 73-77, 99-103, 101-105, 222-226, 359-263

**N-myristoylation site.**

amino acids 8-14, 51-57, 59-65, 69-75, 70-76, 167-173, 173-179, 177-183, 188-194, 250-256, 253-259, 267-273, 280-286, 283-289, 326-332, 372-378, 395-401

**Aspartic acid and asparagine hydroxylation site.**

amino acids 321-333

**EGF-like domain cysteine pattern signature.**

amino acids 181-193

## **FIGURE 41**

TGAGACCCTCCTGCAGCCTCTCAAGGGACAGCCCCACTCTGCCTCTTGCTCCTCCAGGGCA  
GCACCATGCAGCCCCCTGTGGCTCTGCTGGGACTCTGGGTGTTGCCCTGGCCAGCCCCGGG  
GCCGCCCTGACCAGGGGAGCAGCTCCTGGCAGCCTGCTGCCAGCTGAGCTCAAAGAGGT  
GCCCACCCCTGGACAGGGCCGACATGGAGGAGCTGGTCATCCCCACCCACGTGAGGGCCCAGT  
ACGTGGCCCTGCTGCAGCGCAGCCACGGGACCGCTCCCGCGAAAGAGGTTCAGCCAGAGC  
TTCCGAGAGGTGGCCGGCAGGTTCTGGCGTTGGAGGCCAGCACACACCTGCTGGTGGTCTGG  
CATGGAGCAGCGGCTGCCGCCAACAGCGAGCTGGTGCAGGCCGTGCTGCCCTCTCCAGG  
AGCCGGTCCCCAAGGCCGCGCTGCACAGGCACGGGCGGCTGTCCCCGCGCAGGCCCGGGCC  
CGGGTGACCGTCGAGTGGCTGCGCGTCCCGACGACGGCTCCAACCGCACCTCCCTCATCGA  
CTCCAGGCTGGTGTCCGTCCACGAGAGCGGCTGGAAGGGCTTCGACGTGACCGAGGCCGTGA  
ACTTCTGGCAGCAGCTGAGCCGGCCCGGCAGCCGCTGCTGCTACAGGTGTCGGTGCAGAGG  
GAGCATCTGGGCCCGCTGGCGTCCGGCGCCACAAGCTGGTCCGCTTGCCCTCGCAGGGGGC  
GCCAGCCGGCTGGGGAGCCCCAGCTGGAGCTGCACACCCCTGGACCTGGGACTATGGAG  
CTCAGGGCGACTGTGACCCCTGAAGCACCAATGACCGAGGGCACCGCTGCTGCCGCCAGGAG  
ATGTACATTGACCTGCAGGGATGAAGTGGCCGAGAAGTGGGTGCTGGAGCCCCCGGCTT  
CCTGGCTTATGAGTGTGGCACCTGCCGGCAGCCCCCGGAGGCCCTGGCCTTCAAGTGGC  
CGTTTCTGGGGCCTCGACAGTCATGCCCTGGAGACTGACTCGCTGCCCATGATCGTCAGC  
ATCAAGGAGGGAGGCAGGACCAGGCCAGGTGGTCAGCCTGCCAACATGAGGGTGCAGAA  
GTGCAGCTGTGCCTCGGATGGTGCCTCGCAAGGAGGCTCCAGCCATAGGCCCTAGTG  
TAGCCATCGAGGGACTTGACTTGTGTGTTCTGAAGTGTGCTGAGGGTACCAAGGAGAGCTG  
GCGATGACTGAAGTGCATGGACAAATGCTCTGTGCTCTAGTGAGCCCTGAATTGCTT  
CCTCTGACAAGTTACCTCACCTAATTTGCTCTCAGGAATGAGAATCTTGGCCACTGGA  
GAGCCCTGCTCAGTTCTCTATTCTTACTGCACTATATTCTAACGACTTACAT  
GTGGAGATACTGTAACCTGAGGGCAGAAAGCCANTGTGTCATTGTTACTTGTCCGTAC  
TGGATCTGGCTAAAGTCCTCCACCACCTGGACCTAACGACCTGGGTTAAGTGTGGGT  
TGTGCATCCCCAATCCAGATAATAAGACTTTGTAAAACATGAATAAACACATTTATTCT  
AAAA

## **FIGURE 42**

MQPLWLCWALWVLPLASPGAAALTGEQLLGSLLRQLQLKEVPTLDRADMEELVIPTHVRAQYV  
ALLQRSHGDRSRGKRFQSFRREVAGRFLALEASTHLLVFGMEQRLPPNSELVQAVLRLFQEP  
VPKAALHRHGRLSPRSARARVTVEWLRVRDDGSNRTSLIDSRLSVHESGWKAFDVTEAVNF  
WQQLSRPRQPLLLQSVQREHLGPLASGAHKLVRFASQGAPAGLGEPQLELHTLDLGDYGAQ  
GDCDPEAPMTEGTRCCRQEMYIDLQGMKWAENVLEPPGFLAYECVGTCRQPPEALAFKWPF  
LGPRQCIASETDSLPMIVSIKEGGRTRPQVVSLPNMRVQKCSCASDGALVPRRLQP

**Signal sequence:**

amino acids 1-18

**N-glycosylation site.**

amino acids 158-162

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 76-80

**Casein kinase II phosphorylation site.**

amino acids 68-72, 81-85, 161-165, 169-173, 319-323, 329-333

**N-myristoylation site.**

amino acids 19-25, 156-162, 225-231, 260-266, 274-280

**Amidation site.**

amino acids 74-78

**TGF-beta family signature.**

amino acids 282-298

## **FIGURE 43**

GTCTGTTCCCAGGAGTCCTCGCGGCTGTTGTCAGTGGCCTGATCGC**GATGGGGACAAA**  
GGCGCAAGTCGAGAGGAAACTGTTGTCCTCTCATATTGGCGATCCTGTTGCTCCCTGG  
CATTGGGCAGTGTACAGTGCACCTCTGAACCTGAAGTCAGAATTCTGAGAATAATCCT  
GTGAAGTTGTCCTGTCCTACTCGGGCTTTCTTCTCCCCGTGGAGTGGAAAGTTGACCA  
AGGAGACACCACCAAGACTCGTTGCTATAATAACAAGATCACAGCTCCTATGAGGACCGGG  
TGACCTTCTGCCAACTGGTATCACCTCAAGTCCGTGACACGGGAAGACACTGGGACATAC  
ACTTGTATGGTCTCTGAGGAAGGCGAACAGCTATGGGAGGTCAAGGTCAAGCTCATCGT  
GCTTGTGCCTCCATCCAAGCCTACAGTTAACATCCCCTCTGCCACCATTGGGAACCGGG  
CAGTGCTGACATGCTCAGAACAGATGGTCCCCACCTCTGAATAACACACTGGTCAAAGAT  
GGGATAGTGATGCCTACGAATCCAAAAGCACCCGTGCCCTCAGCAACTCTCCTATGTCT  
GAATCCCACACAGGAGAGCTGGTCTTGATCCCCTGTCAAGCTCTGATAACTGGAGAATACA  
GCTGTGAGGCACGGAATGGGTATGGGACACCCATGACTCAAATGCTGTGCGATGGAGCT  
GTGGAGCGGAATGTGGGGTCATCGTGGCAGCCGTCTGTAACCCCTGATTCTCCTGGGAAT  
CTTGGTTTTGGCATCTGGTTGCCTATAGCCGAGGCCACTTGACAGAACAAAGAAAGGGA  
CTTCGAGTAAGAAGGTGATTACAGCCAGCCTAGTGCCGAAGTGAAGGAGAATTCAAACAG  
ACCTCGTCATTCTGGT**GTCAGCCTGGTCGGCTCACCGC**TATCATCTGCATTTGCCTTACT  
CAGGTGCTACGGACTCTGGCCCTGATGTCTGTAGTTCACAGGATGCCCTATTGTCTTC  
TACACCCCACAGGGCCCCCTACTTCTCGGATGTGTTTAATAATGTCAGCTATGCC  
ATCCTCCTTCATGCCCTCCCTCCCTTACCACTGCTGAGTGGCTGGAACTTGTAA  
GTGTTATTCCCCATTCTTGAGGGATCAGGAAGGAATCCTGGGTATGCCATTGACTTCCC  
TTCTAAGTAGACAGAAAAATGGCGGGGTGCAGGAATCTGCACTCAACTGCCACCTGGC  
TGGCAGGGATCTTGAATAGGTATCTTGAGCTGGTTCTGGCTCTTCCTGTACTGAC  
GACCAGGGCCAGCTGTTCTAGAGCGGAATTAGAGGCTAGAGCGGCTGAAATGGTTGG  
TGATGACACTGGGTCTTCCATCTCTGGGCCACTCTCTGTCTTCCATGGGAAGTG  
CCACTGGATCCCTCTGCCCTGTCCCTGAATACAAGCTGACTGACATTGACTGTCTGT  
GGAAAATGGGAGCTTGTGAGAGGCATAGTAAATTTCAGAGAACCTGAAGCCAAAAG  
GATTAAAACCGCTGCTCTAAAGAAAAGAAAAGCTGGAGGCTGGCGCAGTGGCTACGCC  
TAATCCCAGAGGCTGAGGCAGGCGGATCACCTGAGGTGGAGTTGGATCAGCCTGACCA  
ACATGGAGAAACCTACTGGAAATACAAAGTTAGCCAGGCATGGTGGTGCATGCCGTAGTC  
CCAGCTGCTCAGGAGCCTGGCAACAAAGAGCAAAACTCCAGCTAAAAAAAAAAAAAA

## **FIGURE 44**

MGTKAQVERKLLCLFILA ILLCSLALGSVTVHSSEPEVRI PENNPVKLSCAYSGFSSPRVEW  
KFDQGDTTRLCYNNKITASYEDRVTFLPTGITFKSVTREDTGTYTCMVSEEGGNSYGEVKV  
KLIVLVPPSKPTVNIPSSATIGNRAVLTCS EQDGSPPSEYTWFKDGI VMPTNPKSTRAFSNS  
SYVLNPTTGELVFDPLSASDTGEYSCEARNGYGT PMTSNAVRMEAVERNVGVIVAAVLVTLI  
LLGILVFGIWFAYSRGHFDRTKKGTSSKKVIYSQPSARSEGEFKQTSSFLV

**Signal sequence:**

amino acids 1-27

**Transmembrane domain:**

amino acids 238-255

**N-glycosylation site.**

amino acids 185-189

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 270-274

**Casein kinase II phosphorylation site.**

amino acids 34-38, 82-86, 100-104, 118-122, 152-156, 154-158,  
193-197, 203-207, 287-291

**N-myristoylation site.**

amino acids 105-111, 116-122, 158-164, 219-225, 237-243, 256-262

## **FIGURE 45**

CAGCGCGTGGCCGGCGCCGTGTGGGACAGC**A**TGAGCGGCGGTGGATGGCGCAGGTTGGA  
GCGTGGCGAACAGGGCTCTGGCCTGGCGCTGCTGCTGCTCGGCCTCGGACTAGGCCT  
GGAGGCCGCGCGAGCCGCTTCCACCCGACCTCTGCCCAGGCCGCAGGCCAGCTCAG  
GCTCGTGCCAACCAAGTTCCAGTGCCGACCAGTGGCTATGCGTGCCCCTCACCTGG  
CGCTGCGACAGGGACTTGGACTGCAGCGATGGCAGCGATGAGGAGGAGTGCAGGATTGAGCC  
ATGTACCCAGAAAGGGCAATGCCACCGCCCCCTGGCCTCCCTGCCCTGCACCGCGTCA  
GTGACTGCTCTGGGGAACTGACAAGAAACTGCGCAACTGCAGCCGCTGGCCTGCCTAGCA  
GGCGAGCTCCGTTGCACGCTGAGCGATGACTGCATTCCACTCACGTGGCGTGCACGGCCA  
CCCAGACTGTCCCAGCTCCAGCGACGAGCTGGCTGTGGAACCAATGAGATCCTCCGGAAG  
GGGATGCCACAACCATTGGGCCCCCTGTGACCCCTGGAGAGTGTACCTCTCAGGAATGCC  
ACAACCATTGGGCCCCCTGTGACCCCTGGAGAGTGTCCCTCTGTGGAAATGCCACATCCTC  
CTCTGCCGGAGACCAGTCTGGAAGCCA**A**CTGCCTATGGGTTATTGCAGCTGCTGCGGTGC  
TCAGTGCAAGCCTGGTCACCGCCACCCCTCCTCTTTGTCCTGGCTCCGAGCCAGGAGCGC  
CTCCGCCACTGGGTTACTGGTGGCCATGAAGGAGTCCCTGCTGTCA**G**AAACAGAACAGAC  
CTCGCTGCC**T****G**AGGACAAGC**A**CTGCCACCA**C**CGTCACTCACGCCCTGGCGTAGCCGGACA  
GGAGGAGAGCAGTGATGCGGATGGGTACCCGGGACACCCAGCCCTCAGAGACCTGAGTTCTT  
CTGGCCACGTGGAACCTCGAACCCGAGCTCCTGCAGAAGTGGCCCTGGAGATTGAGGGTCCC  
TGGACACTCCCTATGGAGATCCGGGGAGCTAGGATGGGAACCTGCCACAGCCAGAACTGAG  
GGGCTGGCCCCAGGCAGCTCCAGGGGTAGAACGCCCTGTGCTTAAGACACTCCCTGCTG  
CCCCGTCTGAGGGTGGCGATTAAAGTTGCTTC

## FIGURE 46

MSGGWMAQVGAWRTGALGLALLLGLGLGLEAAASPLSTPTSAQAAGPSSGSCPPTKFQCR  
TSGLCVPLTWRCRDLDSDGSDEEECRIEPCTQKGQCPPPGLPCPCTGVSDCSGGTDKKL  
RNCSRRLACLAGELRCTLSDDCIPLTWRCGDGHPCPDSSDELGCGTNEILPEGDATTMGPPVT  
LESVTSLRNATTMGPPVTLESPSVGNATSSSAGDQSGSPTAYGVIAAAAVLSASLVTATLL  
LLSWLRAQERLRPLGLLVAMKESLLLSEQKTSLP

**Signal sequence:**

amino acids 1-30

**Transmembrane domain:**

amino acids 230-246

**N-glycosylation site.**

amino acids 126-130, 195-199, 213-217

**Casein kinase II phosphorylation site.**

amino acids 84-88, 140-144, 161-165, 218-222

**N-myristoylation site.**

amino acids 3-9, 10-16, 26-32, 30-36, 112-118, 166-172, 212-218,  
224-230, 230-236, 263-269

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 44-55

**Leucine zipper pattern.**

amino acids 17-39

## FIGURE 47

CCACACGCGTCCGGTCTCGCTCGCTCGCGCAGCGGCGGCAGCAGAGGTGCGCACAGATGCGG  
GTTAGACTGGCGGGGGAGGAGGAGGAGGGAAAGGAAGCTGCATGCATGAGACCCACAGA  
CTCTTGCAAGCTGGATGCCCTCTGTGGATGAAAGATGTATCATGGAATGAACCCGAGCAATG  
GAGATGGATTCTAGAGCAGCAGCAGCAGCAACCTCAGTCCCCCAGAGACTCTTG  
GCCGTGATCCTGTGGTTCAGCTGGCGCTGTGCTCGGCCCTGCACAGCTCACGGCGGGTT  
CGATGACCTCAAGTGTGCTGACCCGGCATTCCGAGAATGGCTTCAGGACCCCCAGCG  
GAGGGGTTTCTTGAAGGCTCTGTAGCCGATTCACTGCCAAGACGGATTCAAGCTGAAG  
GGCGCTACAAAGAGACTGTGTTGAAGCATTAAATGGAACCTAGGCTGGATCCAAGTGA  
TAATTCCATCTGTGTGCAAGAAGATTGCCGTATCCCTCAAATCGAAGATGCTGAGATTATA  
ACAAGACATATAGACATGGAGAGAAGCTAATCATCACTTGTATGAAGGATTCAAGATCCGG  
TACCCGACCTACACAATATGGTTTATTATGTCGCGATGATGGAACGTGGAATAATCTGCC  
CATCTGTCAAGGCTGCCGTGAGACCTCTAGCCTCTTAATGGCTATGTAACATCTCTGAGC  
TCCAGACCTCTTCCGGTGGGACTGTGATCTCCTATCGCTGCTTCCGGATTAAACTT  
GATGGGTCTGCGTATCTGAGTGCTTACAAAACCTTATCTGGTGTCCAGGCCACCCGGTG  
CCTTGCTCTGGAAGCCAAGTCTGTCCACTACCTCCAATGGTGAGTCACGGAGATTCGTCT  
GCCACCCGGCCCTTGTGAGCGCTACAACCACGGAACGTGGTGGAGTTTACTGCGATCCT  
GGCTACAGCCTCACCAGCGACTACAAGTACATCACCTGCCAGTATGGAGAGTGGTTCTTC  
TTATCAAGTCTACTGCATCAAATCAGAGCAAACGTGGCCAGCACCCATGAGACCCCTCTGA  
CCACGTGGAAGATTGTGGCGTTACGGCAACCAGTGTGCTGCTGGTGTGCTCGTCATC  
CTGGCCAGGATGTTCCAGACCAAGTTCAAGGCCACTTCCCCCAGGGGCTCCCCGGAG  
TTCCAGCAGTGACCTGACTTGTGGTAGACGGCGTGCCTCATGCTCCGTCTATG  
ACGAAGCTGTGAGTGGCGGCTTGAGTGCCTTAGGCCCGGTACATGGCCTCTGTGGCCAG  
GGCTGCCCTTACCGTGGACGACCAGAGCCCCCAGCATAACCCGGCTCAGGGACACGGA  
CACAGGCCAGGGAGTCAGAAACCTGTGACAGCGTCTCAGGCTCTCTGAGCTGCTCCAAA  
GTCTGTATTCACCTCCAGGTGCCAAGAGAGCACCCACCTGCTGGACAACCCGTACATA  
ATTGCCAGCAGGAGGGAGGTGGCATCCACCAAGCCAGGCATCCATGCCACTGGGT  
GTTGTTCTAAGAAACTGATTGATTAAAAATTCCAAAGTGTGCTGAAGTGTCTCTCAA  
ATACATGTTGATCTGTGGAGTTGATTCTTCTCTTGTGGTTAGACAAATGAAACAA  
AGCTCTGATCCTAAAATTGCTATGCTGATAGAGTGGTGGAGGGCTGGAAGCTGATCAAGTC  
CTGTTCTTCTGACACAGACTGATTAAAATTAAAAGNAAAAAA

## **FIGURE 48**

MYHGMNPSNGDGFLEQQQQQQQQSPQRLLAVILWFQLALCFGPAQLTGGFDDLQVCADPGI  
PENGFRTPSGGVFFEGSVARFHCQDGFKLKKGATKRLCLKHFNGTLGWIPSDNSICVQEDCRI  
PQIEDAEIHNKTYRHGEKLIITCHEGFKIRYPDLHNMSLCRDDGTWNNLPLICQGCLRPLAS  
SNGYVNISELQTSFPVGTVISYRCFPGFKLDGSAYLECLQNLIWSSSPRCLALEAQVCPLP  
PMVSHGDFVCHPRPCERYNHGTVEFYCDPGYSLTSYDKYITCQYGEWFPSYQVYCIKSEQT  
WPSTHETLLTTWKIVAFATSVLLVLLVILARMFQTKFKAHFPPRGPPRSSSSDPDFVVVD  
GVPVMLPSYDEAVSGGLSALGPGYMASVGQGCPLPVDDQSPPAYPGSGD'TDTGPGESETCDS  
VSGSSELLQSLYSPPRCQESTHPASDNPDIIASTAEVASTSPGIHHAHWVLFLRN

**Signal sequence:**

amino acids 1-41

**Transmembrane domain:**

amino acids 325-344

**N-glycosylation site.**

amino acids 104-108, 134-138, 192-196

**Casein kinase II phosphorylation site.**

amino acids 8-12, 146-150, 252-256, 270-274, 313-317, 362-366,  
364-368, 380-384, 467-471, 468-472

**N-myristoylation site.**

amino acids 4-10, 61-67, 169-175, 203-209, 387-393, 418-424,  
478-484

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 394-405

## **FIGURE 49**

CCACACGGCTCCGCTCCGCCTCCCCCGCTCCCGTGCCTGCAGCTCCACCGCCGT  
TGCTGCTGCCCGGGTTGCAGTTGTCGCACGCCTCTGCCAGCCAGCCGCTCCACCGCCGT  
AGCGCCGAGTGTCCGGGGCGCACCCGAGTCGGCCATGAGGCCGGAAACCGCGCTACAGG  
CCGTGCTGCCGTGCTGGTGGCTGCCGGCGACGGGTCGCCTGCTGAGTGC  
TCGGATTGGACCTCAGAGGAGGGCAGCCAGTCTGCCGGGAGGGACACAGAGGCCTTGT  
TAAAGTCATTACTTCATGATACTTCTGAAGACTGAACCTTGAGGAAGCAAAGAACCT  
GCAGGAGGGATGGAGGCCAGCTAGTCAGCATCGAGTCTGAAGATGAACAGAAACTGATAGAA  
AAGTCATTGAAAACCTCTGCCATCTGATGGTACTTCTGGATTGGCTCAGGAGGC  
GGAGAAACAAAGCAATAGCACAGCCTGCCAGGACCTTATGCTGGACTGATGGCAGCATAT  
CACAAATTAGGAACGGTATGTGGATGCCGCTGCCGGCAGCGAGGTCTGCGTGGT  
TACCATCAGCCATCGGCACCCGCTGGCATCGGAGGCCCTACATGTTCCAGTGGAAATGATGA  
CCGGTGCAACATGAAGAACAAATTCTTGCAAATATTCTGATGAGAAACCAGCAGTT  
CTAGAGAAGCTGAAGGTGAGGAAACAGAGCTGACAACACCTGTACTTCCAGAAGAACACAG  
GAAGAAGATGCCAAAAAAACATTAAAGAAAGTAGAGAACGCTGCCCTGAATCTGCC  
CCTAATCCCCAGCATTCCCCTCTCCTCCTGTGGTACACAGTTGTATGTTGG  
GGATCTGTAGAAAAAGAAAACGGGAGCAGCCAGACCTAGCACAAAGAACACACC  
TGGCCCTCTCCTCACCAAGGAAACAGCCGGACCTAGAGGTCTACAATGTCATAAGAAA  
AAGCGAAGCTGACTTAGCTGAGACCCGGCCAGACCTGAAGAACATTTCTCGAGTGT  
CGGGAGAAGCCACTCCGATGACATGTCTGTGACTATGACAACATGGCTGTGAACCC  
GAAAGTGGTTGTGACTCTGGTGGAGAGTGGATTGTGACCAATGACATT  
GTTCTCCCCAGACCAATGGGAGGAGTAAGGAGTCTGGATGGTGGAAAATGAA  
GTTATTAGGACATATAAAACTGAAACTGACAACAAATGGAAAAGAAATGATAAGCAAATC  
CTCTTATTTCTATAAGGAAACACAGAAGGTCTATGAACAAAGCTTAGATCAGGT  
GGATGAGCATGTGGCCCCACGACCTCTGGACCCCCACGTTGGCTGTATC  
CCCAGCCAGTCATCCAGCTGACCTTATGAGAACGGTACCTGCCAGGTCTGG  
GAGTCTCAATAATGTCACTTGGTTGGTTGTATCTAAC  
GAGTCTCAATAATGTCACTTGGTTGGTTGTATCTAAC  
GAGTCTCAATAATGTCACTTGGTTGGTTGTATCTAAC  
GCAGTGATAAAAGATGGGCTGTGGAGCTGGAAAACCAC  
CAGCACATATTATCATACAGACAGAAAATCCAGAAC  
GTTGGCCTGTGCATGGCAATTCTCATATCTGTT  
GCAGGAAAAAA

## **FIGURE 50**

MRPGTALQAVLLAVLLVGLRAATGRLLSASDLRGGQPVCRGQTQRPCYKVIYFHDTSRRL  
NFEEAKEACRRDGGQLVSIESEDEQKLIENLLPSDGDFWIGLRRREEKQSNSTACQDL  
YAWTDGSISQFRNWYVDEPSCGSEVCVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNFICKY  
SDEKPAVPSREAEGEETELTPVLPEETQEEDAKKTFKESREAALNAYILIPSIPLLLLLV  
VTTVVCWWICRKRKREQPDPSTKKQHTIWPSPHQGNSPDLEVYNVIRKQSEADLAETRPDL  
KNISFRVCSCGEATPDDMSCDYDNMAVNPSSESGFVTLVSVEGFVTNDIYEFSPDQMGRSKES  
GWVENEIYGY

**Signal sequence:**

amino acids 1-21

**Transmembrane domain:**

amino acids 235-254

**N-glycosylation site.**

amino acids 117-121, 312-316

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 296-300

**Casein kinase II phosphorylation site.**

amino acids 28-32, 30-34, 83-87, 100-104, 214-218, 222-226,  
299-303, 306-310, 323-327

**N-myristoylation site.**

amino acids 18-24, 37-43, 76-82, 146-152

## FIGURE 51

GGGGTCTCCCTCAGGGCCGGAGGCACAGCGGTCCCTGCTGCTGAAGGGCTGGATGTACGC  
ATCCGCAGGTTCCCGCGGACTTGGGGCGCCGCTGAGCCCCGGCGCCCGCAGAAGACTTGT  
GTTTGCCTCCTGCAGCCTCAACCCGGAGGGCAGCGAGGGCCTACCACCAATGATACTGGTGT  
GTTCAGCATGCGCTTGTGGACCCCAGTGGCGTCTGACCTCGCTGGCGTACTGCCTGCACC  
AGCGGCGGGTGGCCCTGGCCGAGCTGCAGGAGGCCATGCCAGTGTCCGGTCACCGCAGC  
CTGCTGAAGTTGAAAATGGTGCAGGTGCTGTTGACACGGGGCTCGGAGTCCTCTCAAGCC  
GCTCCCGCTGGAGGAGCAGGTAGAGTGGAACCCCCAGCTATTAGAGGTCCCACCCAAACTC  
AGTTGATTACACAGTCACCAATCTAGCTGGTGGTCCGAAACCATTCTCCTTACGACTCT  
CAATACCATGAGACCACCCCTGAAGGGGGCATGTTGCTGGCAGCTGACCAAGGTGGCAT  
GCAGCAAATGTTGCCTTGGAGAGAGACTGAGGAAGAACTATGTGGAAAGACATTCCCTTC  
TTTCACCAACCTTCAACCCACAGGAGGTCTTATTGTTCCACTAACATTTCGGAATCTG  
GAGTCCACCCGTTGTTGCTGGCTGGCTTTCCAGTGTCAAGAAAGAAGGACCCATCATCAT  
CCACACTGATGAAGCAGATTAGAAGTCTTGTATCCAACTACCAAAGCTGCTGGAGCCTGA  
GGCAGAGAACCAAGAGGCCGGAGGCAGACTGCCTCTTACAGCCAGGAATCTCAGAGGATTG  
AAAAAGGTGAAGGACAGGATGGCATTGACAGTAGTGTAAAGTGGACTTCTTCATCCTCCT  
GGACAACGTGGCTGCCAGCAGGACACAAACCTCCAAAGCTGCCCATGCTGAAGAGATTG  
CACGGATGATCGAACAGAGAGACTGTGGACACATCCTGTACATACTGCCAAGGAAGACAGG  
GAAAGTCTTCAGATGGCAGTAGGCCATTCCACATCCTAGAGAGCAACCTGCTGAAAGC  
CATGGACTCTGCCACTGCCCGACAAGATCAGAAAGCTGTATCTATGCGGCTCATGATG  
TGACCTTCATACCGCTTTAATGACCCCTGGGATTTGACCACAAATGCCACCGTTGCT  
GTTGACCTGACCATGGAACCTTACCAAGCACCTGGAAATCTAAGGAGTGGTTGTGCAGCTCTA  
TTACCACGGGAAGGAGCAGGTGCCAGAGGTTGCCCTGATGGCTCTGCCGCTGGACATGT  
TCTTGAATGCCATGTCAGTTATACCTTAAGCCCAGAAAAATACCATGCACTCTGCTCTCAA  
ACTCAGGTGATGGAAGTTGGAAATGAAGAGTAACTGATTTATAAAAGCAGGATGTGTTGATT  
TTAAAATAAGTGCCTTATACAATG

## **FIGURE 52**

MITGVFSMRLWTPVGVLTSAYCLHQRRVALAELQEADGQCPVDRSLLKLKMVQVVFRHGAR  
SPLKPLPLEEQVEWNPQLLEVPPQTQFDYTVTNLAGGPKPYSPYDSQYHETTLKGGMFAGQL  
TKVGMQQMFALGERLRKNYVEDIPFLSPTFNPQEVFIRSTNIFRNLESTRCLLAGLFQCQKE  
GPIIIHTDEADSEVLYPNYQSCWSLRQRTRGRRQTASLQPGISEDLKKVKDRMGIDSSDKVD  
FFILLDNVAAEQAHNLPSCPMLKRFARMIEQRAVDTSLYILPKEDRESLQMAVGPFHLILES  
NLLKAMDSATAPDKIRKLYLYAAHDVTIFIPLLMTLGIFDHKWPPFAVDLTMELYQHLESKEW  
FVQLYYHGKEQVPRGCPDGLCP LDMLNAMS VYTLSPEKYHALCSQTQVM EVGNEE

**Signal sequence:**

amino acids 1-23

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 218-222

**Casein kinase II phosphorylation site.**

amino acids 87-91, 104-108, 320-324

**Tyrosine kinase phosphorylation site.**

amino acids 280-288

**N-myristoylation site.**

amino acids 15-21, 117-123, 118-124, 179-185, 240-246, 387-393

**Amidation site.**

amino acids 216-220

**Leucine zipper pattern.**

amino acids 10-32

**Histidine acid phosphatases phosphohistidine signature.**

amino acids 50-65

## **FIGURE 53**

CTCCTCTAACATACTTGCAGCTAAAACATAATGGCTGCTGGGGACCTCCTCTAGCCT  
TAAATTCAGCTCATCACCTCACCTGCCTTGGTCAATGGCTCTGCTATTCTCCTGATCCTT  
GCCATTTGCAACCAGACCTGGATTCTAGCGTCTCCATCTGGAGTGCGGCTGGTGGGGGCT  
CCACCGCTGTGAAGGGCGGGTGGAGGTGGAACAGAAAGGCCAGTGGGGCACC GTGTGATG  
ACGGCTGGGACATTAAGGACGTGGCTGTGTTGCCGGAGCTGGCTGTGGAGCTGCCAGC  
GGAACCCCTAGTGGTATTTGTATGAGCCACCAGCAGAAAAAGAGCAAAAGGTCTCATCCA  
ATCAGTCAGTTGCACAGGAACAGAAGATACTGGCTCAGTGTGAGCAAGAAGAAGTTATG  
ATTGTTCACATGATGAAGATGCTGGGCATCGTGTGAGAACCCAGAGAGCTTTCTCCCCA  
GTCCCAGAGGGTGTCAAGGCTGGCTGACGCCCTGGCATTGCAAGGGACCGTGGAGTGAA  
GCACCAGAACCAAGTGGTATACCGTGTGCCAGACAGGCTGGAGCCTCCGGCCGAAAGGTGG  
TGTGCCGGCAGCTGGGATGTGGGAGGGCTGTACTGACTCAAAACGCTGCAACAAGCATGCC  
TATGGCCGAAAACCATCTGGCTGAGCCAGATGTCATGCTCAGGACGAGAAGCAACCCTCA  
GGATTGCCCTCTGGCCTTGGGAAAGAACACCTGCAACCATGATGAAGACACGTGGTCG  
AATGTGAAGATCCCTTGACTTGAGACTAGTAGGAGGAGACAACCTCTGCTCTGGCGACTG  
GAGGTGCTGCACAAGGGCGTATGGGCTCTGTCTGTGATGACAACGGGAGAAAAGGAGGA  
CCAGGTGGTATGCAAGCAACTGGCTGTGGAAGTCCCTCTCCCTCAGAGACCGGA  
AATGCTATGCCCTGGGTTGGCCGATCTGGCTGGATAATGTCGTTGCTCAGGGAGGAG  
CAGTCCCTGGAGCAGTGC CAGCACAGATTTGGGGTTTCACGACTGCACCCACCAGGAAGA  
TGTGGCTGTCATCTGCTCAGTGTAGGTGGCATCATCTAATCTGTTGAGTGCTGAATAGAA  
GAAAAACACAGAAGAAGGGAGCATTACTGTCTACATGACTGCATGGATGAACACTGATCT  
TCTTCTGCCCTGGACTGGACTTATACTTGGTGCCTGATTCTCAGGCCCTCAGAGTTGG  
ATCAGAACTTACAACATCAGGTCTAGTTCTCAGGCCATCAGACATAGTTGGAACATACATCA  
CCACCTTCCTATGTCACATTGCACACAGCAGATTCCAGCCTCCATAATTGTGTGTAT  
CAACTACTAAATACATTCTCACACACACACACACACACACACACACACACACACATA  
CACCAATTGTCCTGTTCTGTGAAGAACTCTGACAAAATACAGATTTGGTACTGAAAGAGA  
TTCTAGAGGAACGGAATTAAAGGATAAATTCTGAATTGGTTATGGGTTCTGAAATTG  
GCTCTATAATCTAATTAGATAAAAATTCTGGTAACTTATTACAATAATAAGATAGCAC  
TATGTGTTAAA

## **FIGURE 54**

MALLFSLILAICTRPGLASPSGVRLVGGHLRCEGRVEQKGQWGTVCDDGWDIKDVAVLC  
RELGCGAASGTPSGILYEPPAEKEQKVLIQSVSCTGTEDTLAQCEQEEVYDCSHDEDAGASC  
ENPESSFSPVPEGVRLADGPGHCKGRVEVKHQNQWYTCQTGWSLRAAKVVCRQLGCGRAVL  
TQKRCNKHAYGRKPIWLSQMCSGREATLQDCPSGPWGKNTCNHDEDTWECEDPFDLRLVG  
GDNLCSGRLEVLHKGVWGSVCDDNWGEKEDQVVCKQLGCGKSLSPSFRDRKCYGPGVGRIDL  
DNVRCSGEEQSLEQCQHRFWGFHDCTHQEDVAVICSV

**Signal sequence:**

amino acids 1-15

**Casein kinase II phosphorylation site.**

amino acids 47-51, 97-101, 115-119, 209-213, 214-218, 234-238,  
267-271, 294-298, 316-320, 336-340

**N-myristoylation site.**

amino acids 29-35, 43-49, 66-72, 68-74, 72-78, 98-104, 137-143,  
180-186, 263-269, 286-292

**Amidation site.**

amino acids 196-200

**Speract receptor repeated domain signature.**

amino acids 29-67, 249-287

## **FIGURE 55**

ACTGCACTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTGACCTCGAC  
CCACCGCGTCCCGCGACCGCGTGGCGGACCGCGTGGGCCGGCTACCAGGAAGAGTCTGCCGAAG  
GTGAAGGCCATGGACTTCATCACCTCCACAGCCATCCTGCCCTGCTGTCGGCTGCCTGGG  
CGTCTTCGGCCTCTCCGGCTGCTGCAGTGGGTGCGCGGGAAAGGCCTACCTGCAGGAATGCTG  
TGGTGGTGATCACAGGCGCCACCTCAGGGCTGGCAAAGAATGTGAAAAGTCTTATGCT  
GCGGGTGCTAAACTGGTGCTCTGTGGCCGGAAATGGTGGGCCCTAGAAGAGCTCATCAGAGA  
ACTTACCGCTTCTCATGCCACCAAGGTGCAGACACACAAGCCTACTTGGTGACCTTCGACC  
TCACAGACTCTGGGCCATAGTTGCAGCAGCAGCTGAGATCCTGCAGTGCTTGCTATGTC  
GACATACTTGTCAACAATGCTGGATCAGCTACCGTGGTACCATCATGGACACCAAGTGG  
TGTGGACAAGAGGGTCATGGAGACAAACTACTTGGCCCAGTTGCTCTAACGAAAGCACTCC  
TGCCCTCCATGATCAAGAGGGAGGAAGGCCACATTGTCGCCATCAGCAGCATCCAGGGCAAG  
ATGAGCATTCTTTGATCAGCATATGCAGCCTCCAAGCACGCAACCCAGGCTTCTTGA  
CTGTCGCGTGCCGAGATGGAACAGTATGAAATTGAGGTGACCGTCATCAGCCCCGGCTACA  
TCCACACCAACCTCTGTAAATGCCATCACCAGGATGGATCTAGGTATGGAGTTATGGAC  
ACCACCCACAGCCCAGGGCGAAGCCCTGTGGAGGTGGCCAGGATGTTCTGCTGCTGTGGG  
GAAGAAGAAGAAAGATGTGATCCTGGCTGACTTACTGCCTTCAGGGCAGAAAAGAGCGGAAATCC  
AAGAACTCCTAGTACTCTGACCAGCCAGGGCAGGGCAGAGAAGCAGCACTCTTAGGCTTGC  
TTACTCTACAAGGGACAGTTGCATTGAGACTTTAATGGAGATTGTCTCACAAGTGG  
AAAGACTGAAGAAACACATCTCGTGCAGATCTGCTGGCAGAGGACAATAAAAACGACAACA  
AGCTTCTTCCCAGGGTGAGGGAAACACTTAAGGAATAATGGAGCTGGGTTAACACT  
AAAAACTAGAAATAAACATCTCAAACAGTAAAAAAAAAAAGGGCGGCCGCGACTCTAG  
AGTCGACCTGCAGAAGCTTGGCCGCCATGGCCCAACTTGTATTGCAGCTTATAATGGTTAC

## **FIGURE 56**

MDFITSTAILPLLFGCLGVFGLFRLLQWVRGKAYLRNAVVIITGATSGLGKECAKVFYAAGA  
KLVLCGRNGGALEELIRELTASHATKVQTHKPYLVTFDLTDGAI  
VAAAEEILQCFGYVDIL  
VNNAGISYRGTIMDTTVDVDKRVMETNYFGPVALTKALLPSMIKRRQGHIVAISSIQGKMSI  
PFRSAYAASKHATQAFFDCLRAEMEQYEIEVTVISPGYIHTNLSVNAITADGSRYGVMDTTT  
AQGRSPVEVAQDVLAAGKDDVILADLLPSLAVYLRTLAPGLFFSLMASRARKERKS KNS

**Signal sequence:**

amino acids 1-21

**Transmembrane domain:**

amino acids 104-120, 278-292

**N-glycosylation site.**

amino acids 228-232

**Glycosaminoglycan attachment site.**

amino acids 47-51

**Casein kinase II phosphorylation site.**

amino acids 135-139, 139-143, 253-257

**Tyrosine kinase phosphorylation site.**

amino acids 145-153, 146-153

**N-myristoylation site.**

amino acids 44-50, 105-111, 238-244, 242-248, 291-297

**Amidation site.**

amino acids 265-269

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 6-17

## FIGURE 57

CCACAGCGTCCGCTGGTGTAGATCGAGCAACCCCTAAAGCAGTTAGAGTGGTAAAAAA  
AAAAAAAAACACACCAACGCTCGCAGCCACAAAGGGATGAATTCTGGACATCCTC  
CTGCTTCTCCCGTTACTGATCGTCTGCTCCCTAGAGTCCTCGTGAAGCTTTTATTCTAA  
GAGGAGAAAATCAGTCACCGCGAAATCGTGTGATTACAGGAGCTGGCATGGAATTGGGA  
GAUTGACTGCCTATGAATTGCTAAACTAAAGCAAGCTGGTCTCTGGATATAAATAAG  
CATGGACTGGAGGAAACAGCTGCCAAATGCAAGGGACTGGTGCCTAGGTTACACCTTGT  
GGTAGACTGCAGCAACCGAGAAGATATTACAGCTCTGCAAAGAAGGTGAAGGCAGAAATTG  
GAGATGTTAGTATTTAGTAAATAATGCTGGTAGTCTATACATCAGATTGTTGCTACA  
CAAGATCCTCAGATTGAAAAGACTTTGAAGTTAATGTACTTGACACATTCTGGACTACAAA  
GGCATTCTCCTGCAATGACGAAGAATAACCATTGCCATATTGTCAGTGGCTCGGCAG  
CTGGACATGTCTCGGTCCCTCTTACTGGCTACTGTTCAAGCAAGTTGCTGTTGGA  
TTTCATAAAACTTGACAGATGAACTGGCTGCCTACAAATACTGGAGTCAAAACACATG  
TCTGTGTCCTAATTCGTAAACACTGGCTTCATCAAAATCCAAGTACAAGTTGGACCCA  
CTCTGGAACCTGAGGAAGTGGTAAACAGGCTGATGCATGGATTCTGACTGAGCAGAAGATG  
ATTTTATTCCATCTTCTATAGCTTTTAACAACATTGAAAGGATCCTCCTGAGCGTTT  
CCTGGCAGTTTAAAACGAAAAATCAGTGTAAAGTTGATGCAGTTATTGGATATAAAATGA  
AAGCGCAATAGCACCTAGTTCTGAAAATGATTACAGGTTAGGTTGATGTCATCTA  
ATAGTGCAGAATTAAATGTTGAACTTCTGTTTTCTAATTATCCCCATTCTCAATA  
TCATTTTGAGGCTTGGCAGTCTCATTACTACCACTTGTCTTAGCCAAAGCTGATT  
ACATATGATATAAACAGAGAAATACCTTAGAGGTGACTTAAGGAAATGAAGAAAAGAA  
CCAAAATGACTTTATTAAATAATTCCAAGATTATTGTTGACTGAAAGGCTTGC  
AATTGTACCATACCGTTATTAAACATATAATTATTATTGATTGACTTAAATTGTTG  
ATAATTGTGTTCTTTCTGTTCTACATAAAATCAGAAACTTCAGCTCTCTAAATAAAA  
TGAAGGACTATATCTAGGGTATTCAACATGAATATCATGAACTCTCAATGGTAGGTT  
ATCCTACCCATTGCCACTCTGTTCTGAGAGATACCTCACATTCAATGCCAAACATTCT  
GCACAGGGAAGCTAGAGGTGGATACACGTGTGCAAGTATAAAAGCATCACTGGATT  
GAGAATTGAGAGAATGTACCCACAAATGGCAGCAATAATAAATGGATCACACTTAA  
AAA  
AAA

## **FIGURE 58**

MKFLLDILLPLLLIVCSLESFVKLFIPKRRKSVTGEIVLITGAGHIGRLTAYEFAKLKSK  
LVLWDINKHGLEETAACKGLGAKVHTFVVDCSNREDIYSSAKVKAEIGDVSILVNNAGVV  
YTSDLFATQDPQIEKTFEVNVLAHFWTTKAFLPAMTKNNHGHIVTVASAAGHVSVPFLLAYC  
SSKFAAVGFHKTLTDELAALQITGVKTTCLCPNFVNTGFIKNPSTSLGPTLEPEEVVNRLMH  
GILTEQKMIFIPSSIAFLTTLERILPERFLAVLKRKISVKFDAVIGYKMKAQ

**Signal sequence:**

amino acids 1-19

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 30-34, 283-287

**Casein kinase II phosphorylation site.**

amino acids 52-56, 95-99, 198-202, 267-271

**N-myristoylation site.**

amino acids 43-49, 72-78, 122-128, 210-216

## **FIGURE 59**

CCACCGCGTCCGGACCGTGGTCGACTAGTTAGATCGCGAGCGGCCGCCGGCTC  
AGGGAGGAGCACCAGCTGCGCCGCACCTGAGAGATGGTGGTGCCATGTGGAAGGTGATTG  
TTTCGCTGGTCCTGTTGATGCCCTGGCCCTGTGATGGCTGTTCGCTCCCTATACAGAAAGT  
GTTCCATGCCACCTAAGGGAGACTCAGGACAGCATTATTCCTCACCCCTTACATTGAAGC  
TGGGAAGATCCAAAAGGAAGAGAATTGAGTTGGTCCGGCTTCCCAGGACTGAACATGA  
AGAGTTATGCCGGCTCCTCACCGTGAATAAGACTTACAACAGCAACCTCTTCTGGTTC  
TTCCCAGCTCAGATACAGCCAGAAGATGCCAGTAGTTCTGGCTACAGGGTGGGCCGGG  
AGGTTCATCCATGTTGGACTCTTGTGGAACATGGCCCTATGTTGTACAAGTAACATGA  
CCTTGCCTGACAGAGACTTCCCCTGGACCACAACGCTCTCCATGCTTACATTGACAATCCA  
GTGGGCACAGGCTTCAGTTACTGATGATAACCACGGATATGCAGTCATGAGGACGATGT  
AGCACGGGATTATACAGTGCACTAATTCAAGTTTCAGATAATTCTGAATAATAAAAATA  
ATGACTTTATGTCACTGGGAGTCTTATGCAGGGAAATATGTGCCAGCCATTGCACACCTC  
ATCCATTCCCTCAACCCCTGTGAGAGAGGTGAAGATCAACCTGAACGGAATTGCTATTGGAGA  
TGGATATTCTGATCCGAATCAATTATAGGGGCTATGCAGAAATTCTGTACCAAATTGGCT  
TGTTGGATGAGAAGCAAAAAAGTACTCCAGAAGCAGTGCATGAATGCATAGAACACATC  
AGGAAGCAGAACTGGTTGAGGCCTTGAAATACTGGATAAAACTACTAGATGGCAGTTAAC  
AAAGTGCATCCCTTACTTCCAGAATGTTACAGGATGTAGTAATTACTATAACTTTGCGGT  
GCACGGAACTGAGGATCAGCTTACTATGAAATTGTCACTCCCAGAGGTGAGACAA  
GCCATCCACGTGGGAATCAGACTTTAATGATGAACTATAGTGAAGAAGTACTTGCAGA  
AGATACAGTACAGTCAGTTAAGCCATGGTTAAGTAACTGAAATCATGAATAATTAAAGGTTCTGA  
TCTACAATGCCAAGTGGACATCATCGTGGCAGCTGCCCTGACAGAGCGCTCCTGATGGC  
ATGGACTGGAAAGGATCCCAGGAATACAAGAAGGCAGAAAAAAAGTTGGAAGATCTTAA  
ATCTGACAGTGAAGTGGCTGGTTACATCCGGCAAGCGGGTGACTTCCATCAGGTAATTATTC  
GAGGTGGAGGACATATTTACCCATGACCAGCCTCTGAGAGCTTGACATGATTAATCGA  
TTCATTATGGAAAAGGATGGATCCTTATGGATAAAACTACCTCCAAAAGAGAACAT  
CAGAGGTTTCATTGCTGAAAAGAAAATCGAAAAACAGAAAATGTCATAGGAATAAAAAAA  
TTATCTTTCATATCTGCAAGATTTTTCATCAATAAAAATTATCCTGAAACAAGTGAGC  
TTTGTTTTGGGGGAGATGTTACTACAAATTAAACATGAGTACATGAGTAAGAATTACA  
TTATTTAACTAAAGGATGAAAGGTATGGATGATGTGACACTGAGACAAGATGTATAATGA  
AATTAGGGCTTGAATAGGAAGTTTAATTCTCTAAGAGTAAGTGAAGAAGTGCAGTTG  
TAACAAACAAAGCTGTAACATCTTCTGCCAATAACAGAAGTTGGCATGCCGTGAAGGT  
GTTTGGAAATATTATGGATAAGAATAGCTCAATTATCCAAAATAAATGGATGAAGCTATAA  
TAGTTTGGGGAAAAGATTCTCAAATGTATAAAGTCTTAGAACAAAAGAATTCTTGAAATA  
AAAATATTATATAAAAGTAAAAAA

## **FIGURE 60**

MVGAMWKVIVSLVLLMPGCDGLFRSLYRSVSMPKGDSGQPLFLTPYIEAGKIQKGREL  
SLVGPPGLNMKSYAGFLTVNKTYNSNLFFWFFPAQIQPEDAPVVLWLQGGPGGSSMFGLFVEH  
GPYVVTTSNMTLRDRDFPWTTLSMLYIDNPVGTGFSFTDDTHGYAVNEDDVARDLYSALIQF  
FQIFPEYKNNDFYVTGESYAGKYVPAIAHLIHSNLPREVKINLNGIAIGDGYSDPESIIGG  
YAEFLYQIGLLDEKQKKYFQKQCHECIEHIRKQNWFEAFEILDKLLGDLTSDPSYFQNVTG  
CSNYYNFLRCTEPEDQLYYVKFLSLPEVRQAIHVGQTFNDGTIVEKYLREDTVQSVKPWLT  
EIMNNYKVLIYNGQLDIIVAALTERSLMGMDWKGSQEYKKAEKVKWKFSDSEVAGYIRQ  
AGDFHQVIIRGGGHILPYDQPLRAFDMINRFIYGKGWDPYVG

**Signal sequence:**

amino acids 1-22

**N-glycosylation site.**

amino acids 81-85, 132-136, 307-311, 346-350

**Casein kinase II phosphorylation site.**

amino acids 134-138, 160-164, 240-244, 321-325, 334-338, 348-352,  
353-357, 424-428

**Tyrosine kinase phosphorylation site.**

amino acids 423-432

**N-myristoylation site.**

amino acids 22-28, 110-116, 156-162, 232-238

**Serine carboxypeptidases, serine active site.**

amino acids 200-208

**Crystallins beta and gamma 'Greek key' motif signature.**

amino acids 375-391

## FIGURE 61

CGAGGGCTTTCCGGCTCCGAATGGCACATGTGGGAATCCCAGTCTTGTGGCTACAACAT  
TTTCCCTTCTAACAAAGTTCTAACAGCTGTTCTAACAGCTAGTGTACAGGGGTTCTTCTT  
GCTGGAGAAGAAAGGGCTGAGGGCAGAGCAGGGCACTCTCACTCAGGGTGACCAGCTCCTTG  
CCTCTCTGTGGATAACAGAGCATGAGAAAGTGAAGAGATGCAGCGGAGTGAGGTGATGGAAG  
TCTAAAATAGGAAGGAATTGTGTGCAATATCAGACTCTGGGAGCAGTGACCTGGAGAGC  
CTGGGGGAGGGCCTGCCTAACAAAGCTTCAAAAAACAGGAGCGACTTCACTGGCTGGGAT  
AAGACGTGCCGGTAGGGATAGGGAAAGACTGGGTTAGTCCTAACATATCAAATTGACTGGCTGGG  
TGAACCTCAACAGCCTTTAACCTCTGGGAGATGAAAACGATGGCTTAAGGGGCCAGAAA  
TAGAGATGCTTGTAAAATAAAATTAAAAAGCAAGTATTATAGCATAAAGGCTAGA  
GACCAAAATAGATAACAGGATTCCCTGAACATTCTAACAGGAGGAAAGTATGTTAAAATA  
GAAAAACAAAATGCAGAAGGAGGAGACTCACAGAGCTAACCCAGGATGGGACCCCTGGGTC  
AGGCCAGCCTTTGCTCCTCCGGAAATTATTTGGTCTGACCACTCTGCCTTGTGTTT  
GCAGAATCATGTGAGGGCAACCGGGGAAGGTGGAGCAGATGAGCACACACAGGAGCCGTCT  
CCTCACCGCCGCCCTCTCAGCATGGAACAGAGGCAGCCCTGGCCCCGGGCCCTGGAGGTGG  
ACAGCCGCTCTGTGGTCTCTCAGTGGCTGGGTGCTGCTGGCCCCCAGCAGCCGGC  
ATGCCCTCAGTTCAGCACCTTCACTCTGAGAACATCGTACTGGACCTCAACCACCTGACCGT  
CCACCAAGGGACGGGGCGTCTATGTGGGGCCATCAACCGGGTCTATAAGCTGACAGGCA  
ACCTGACCATCCAGGTGGCTATAAGACAGGGCAGAACAGGACAACAAGTCTCGTTACCCG  
CCCTCATCGTGCAGCCCTGAGCGAAGTGCTCACCCCTACCAACAATGTCAACAAGCTGCT  
CATCATTGACTACTCTGAGAACCGCCCTGCTGGCCTGTGGAGCCTCTACCAGGGGTCTGCA  
AGCTGCTGGGCTGGATGACCTCTTCATCCTGGTGGAGCCATCCCACAAGAAGGAGCACTAC  
CTGTCCAGTGTCAACAAGACGGGACCATGTACGGGTGATTGTGCGCTCTGAGGGTGAGGA  
TGGCAAGCTTTCATCGGCACGGCTGTGGATGGGAAGCAGGATTACTTCCGACCCCTGTCCA  
GCCGGAAAGCTGCCCCGAGACCCCTGAGTCCTCAGCCATGCTGACTATGAGCTACACAGCGAT  
TTTGTCTCCTCTCATCAAGATCCCTCAGACACCCCTGGCCCTGGTCTCCCACCTTGACAT  
CTTCTACATCTACGGCTTGTAGTGGGGCTTGTCTACTTCTCACTGTCCAGCCGAGA  
CCCTGAGGGTGTGGCCATCAACTCCGCTGGAGACCTCTTACACCTCACGCATCGTGC  
CTCTGCAAGGATGACCCCAAGTTCACTCATACTGTGTCCTGCCCTGGCTGCAACCGGGC  
CGGGGTGGAATACCGCCTCTGAGGCTGCTTACCTGGCCAAGCCTGGGACTCACTGGCC  
AGGCCTTCAATATCACCAGCCAGGACGATGTACTCTTGCCATCTTCTCAAAGGGCAGAAG  
CAGTATCACCACCCGCCGATGACTCTGCCCTGTGCTTACACGGCTACAGCGTGGTTTG  
GCAGATCAAGGAGCGCCTGCAGTCTGCTACCAGGGCAGGGCAACCTGGAGCTCAACTGGC  
TGCTGGGAAGGACGTCCAGTGCACGAAGGCGCTGCCCCATCGATGATAACTCTGTGGA  
CTGGACATCAACCAGCCCTGGGAGGCTCAACTCCAGTGGAGGGCTGACCCCTGTACACCAC  
CAGCAGGGACCGCATGACCTCTGTGGCCTCTACGTTACAACGGCTACAGCGTGGTTTG  
TGGGGACTAAGAGTGGCAAGCTGAAAAAGGTAAGAGTCTATGAGTTGAGCTACAGCTCAATGCC  
ATTCACCTCCTCAGCAAAGAGTCCCTTTGGAAGGTAGCTATTGGTGGAGATTTAACTATAG  
GCAACTTATTTCTGGGAACAAAGGTGAATGGGGAGGTAAGAAGGGTTAATTTGTG  
ACTTAGCTCTAGCTACTCCTCCAGCCATCAGTCATTGGTATGTAAGGAATGCAAGCGTA  
TTCAATATTCCAAACTTAAGAAAAACTTAAGAAGGTACATCTGCAAAAGCAAA

## **FIGURE 62**

MGTLGQASLFAPPGNYFWSDHSALCFAESCEGQPGKVEQMSTHRSRLTAAPLSMEQRQPWP  
RALEVDSRSVVLSSVVWVLLAPPAAGMPQFSTFHSENRDWTFNHLTVHQGTGAVYVGAINRV  
YKLTGNLTIQVAHKTGPEEDNKSRYPPLIVQPCSEVLTLTNNVNKLIIIDYSENRLLACGSL  
YQGVCKLLRLDDLFIILVEPSHKKEHYLSSVNKTGTMGVIVRSEGEDGKLFIGTAVDGKQDY  
FPTLSSRKLPRDPESSAMLDYELHSDFVSSLIKIPLSDTLALVSHFDIFYIYGFASGGFVYFL  
TVQPETPEGVAINSAGDLFYTSRIVRLCKDDPKFHSYVSLPFGCTRAGVEYRLLQAAYLAKP  
GDSLAQAFNITSQDDVLFAIFSKGQKQYHHPPDDSALECAFPIRAINLQIKERLQSCYQGEGN  
LELNWLLGKDVQCTKAPVPIDDNFCGLDINQPLGGSTPVEGLTLYTTSRDRMTSVASYVYNG  
YSVVFGTKSGKLKKVRVYEFRCSNAIHLLSKESLLEGSYWWRFNYRQLYFLGEQR

**Signal sequence:**

amino acids 1-32

**Transmembrane domain:**

amino acids 71-87

**N-glycosylation site.**

amino acids 130-134, 145-149, 217-221, 381-385

**Casein kinase II phosphorylation site.**

amino acids 139-143, 229-233, 240-244, 291-295, 324-328, 383-387,  
384-388, 471-475, 481-485, 530-534

**N-myristylation site.**

amino acids 220-226, 319-325, 353-359, 460-466, 503-509

## FIGURE 63

AGGCTCCCGCGCGCGGCTGAGTGGACTGGAGTGGAAACCCGGGCCCCCGCTTAGAGAACACGCCATGACCA  
CGTGGAGCCTCCGGGGAGGCCGGCCCGCACCGCTGGACTCCCTGCTGGCTTGGGCTCTGGCTCC  
GCAGGGCTGGACTGGAGCACCCCTGGTCCCTGCGGCTCCGCATCGACAGCTGGGCTGCAGGCCAAGGGCTGA  
ACTTCATGCTGGAGGATTCCACCTCTGGATCTCGGGGCTCCACTATTTCCGTGTGCCAGGGAGTACT  
GGAGGGACCCGCTGCTGAAGATGAAGGCTGTGGCTTAACACCCCTCACCACTATGTTCCGTGAAACCTGCATG  
AGCCAGAAAGAGGCAAATTGACTTCTCTGGGAACCTGGACCTGGAGGCCTTCGTCCTGATGGCCGAGAGATCG  
GGCTGGGTGATTCTGCGTCCAGGCCCTACATCTGCACTGAGATGGACCTCGGGGCTTGCCAGCTGGCTAC  
TCCAAGACCTGGCATGAGGCTGAGGACAACATTACAAGGGCTCACCGAAGCAGTGGACCTTATTGACCAC  
TGATGTCAGGGTGGTCCACTCCAGTACAAGCGTGGGGACCTATGCGTGCAGGTGGAGAATGAATATG  
GTTCTATAATAAAAGACCCGCATACATGCCCTACGTCAAGAAGGCACTGGAGGACCGTGGCATTGTTGAACCTGC  
TCCTGACTTCAGACAACAAGGATGGGCTGAGCAAGGGGATTGTCAGGGACTCTGGCCACCATCAACTTGCACT  
CAACACACGAGCTGCAGCTACTGACCACCTTCTCTCAACGTCAGGGACTCAGGCCAACATGGTGTGGAGT  
ACTGGACGGGGTGGTTGACTCGTGGGAGGCCCTACAATATCTGGATTCTCTGAGGTTTGAAAACCGTGT  
CTGCCATTGTGGACGCCGCTCCATCAACCTCTACATGTTCCACGGAGGCCAACATTGGCTTCATGAATG  
GAGCCATGCACTCCATGACTACAAGTCAGATGTCACCGAGCTATGACTATGATGCTGTGACAGAACGGCG  
ATTACACGGCCAAGTACATGAAGCTCGAGACTTCTGGCTCCATCTCAGGCATCCCTCTCCCTCCCCACCTG  
ACCTTCTCCCAAGATGCCGTATGAGCCCTAACGCCAGTCTGTACCTGTCCTGTGGACGCCCTCAAGTACC  
TGGGGAGCCAATCAAGTCTGAAAAGCCATCAACATGGAGAACCTGCCAGTCATGGGGAAATGGACAGTCC  
TCGGGTACATTCTCTATGAGACCAGCATCACCTCGTCTGGCATCCTCAGTGGCACGTGATGTCAGGGCAGG  
TGTTGTGAACACAGTATCCATAGGATTCTGGACTACAAGACAACGAAGATTGCTGTCCCCCTGATCCAGGGTT  
ACACCGTGTGAGGATCTGGTGGAGAATCGTGGCGAGTCACATGGGAGAATATTGATGACCAAGCGCAAAG  
GCTTAATTGAAATCTCTATCTGAATGATTCAACCCCTGAAAAACTTCAGAATCTATAGCCTGGATATGAAGAAGA  
GCTTCTTCAGAGGTTGCCCTGGACAAATGGNNTCCCTCCAGAAACACCCACATTACCTGCTTCTTCTGG  
GTAGCTTGTCCATCAGCTCCACGCCCTGTGACACCTTCTGAAGCTGGAGGGCTGGAGAAGGGGTTGTATTCA  
TCAATGGCCAGAACCTGGACGTTACTGGAACATTGGACCCAGAACAGCCTTACCTCCAGGTCCCTGGTGA  
GCAGCGGAATCAACCAGGTACCGTTTGAGGAGACGATGGCGGCCCTGCATTACAGTCACGGAAACCCCCC  
ACCTGGGAGGAACCAAGTACATTAGTGAAGGGCTGGCACCCCTCTGCTGGTGCAGTGGAGACTGCCGCTC  
CTCTTGTGACCTGAAGCCTGGCTGCTGCCACCCCTCACTGCAAAAGCATCTCTTAAGTAGCAACCTCAGGG  
ACTGGGGGCTACAGTCTGCCCTGTCTCAGTCAAAACCTAACGCTGCAGGAAAGGTGGATGGCTCTGGGCC  
TGGCTTGTGATGATGGCTTCTACAGCCCTGCTTGTGCGAGGCTGTGGCTCTAGGGTGGAGC  
AGCTAATCAGATGCCACGCCCTTGCCCTCAGAAAAAGTGTGAAACAGTGCCTTGACCCGACGTACAGCCC  
TGCGAGCATCTGCTGGACTCAGCGTGCTCTTGCTGGTCTGGGAGGCTGGCCACATCCCTCATGGCCCCAT  
TTTATCCCCGAATCCTGGGTGTGTCACCAGTGTAGAGGGTGGGAAAGGGGTGTCACCTGAGCTGACTTTGTT  
CTTCCCTCACACCTCTGAGCCTTCTTGGGATTCTGGAGGAACCTGGCTGAGAAACATGTGACTTCCCCCT  
TCCCTCCCACTCGCTGCTTCCACAGGGTGACAGGCTGGGCTGGAGAAACAGAAATCCTCACCTGCGTCTCC  
CAAGTTAGCAGGTGCTCTGGTGTGTCAGTGAGGAGGACATGTGAGTCCTGGCAGAACGCCATGGCCATGTCTGCA  
CATCCAGGGAGGAGGACAGAACGGCCAGCTCACATGTGAGTCCTGGCAGAACGCCATGGCCATGTCTGCAACATCC  
AGGGAGGAGGACAGAACGGCCAGCTCACATGTGAGTCCTGGCAGAACGCCATGGCCATGTCTGCAACATCCAGGG  
GGAGGACAGAACGGCCAGCTCACATGTGAGTCCTGGCAGAACGCCATGGCCATGTCTGCAACATCCAGGGAGGAGG  
ACAGAACGGCCAGCTCAGTGGCCCCGCTCCCCACCCCCCAGGCCAACAGCAGGGGAGGAGCAGGCCCTCCTC  
GAAGTGTGTCAGTCCGATTGAGCCTGTTCTGGGGCCAGCCAAACACCTGGCTTGGCTACTGTCTGA  
GTTGCAGTAAAGCTATAACCTTGAATCACAA

## **FIGURE 64**

MTTWSLRRR PARTLGLLLL VV LGFLV LRR LDW STLVPL RL RHQQL GLQAK GWN FM LED STFW  
I FGGS I HYFR VP REYWR DR LLK MKAC GLN T LTY VP WNL HEP ERG KF DF SG NLD LEAF VIL MA  
AEI GLW VILR PG PYIC SEM DLG GLP SW LLQD PG MRL RT TYKG FTEA VD LYFD HLM S RVV PLQ  
YK RGG PI I AVQ VEN EYGS YN KDP AYMP YV KKA LED RGI VELL L TS DN KDG LSK GIV QGV LAT  
IN LQ STHE LQ LTT F L FN VQ GT QPK MVMEY WT GWF D SW GG PHN I LD S SEV LK TV SAI VD AGS  
S IN LYMF HGG TNFG FMNG AMHF HDY KSD VTS YD YDA VL TEA GDY TAKY MKL RD FFG SIS GIP  
L PPPP D L L P KMP Y EPL TP VLY LSL W DALK YL GE PI KSE K P IN M EN L P V N G GNG QSF GY I LY E  
T SIT SSG I LSG H VHD RGQ V FV NTV S I GFL DY KTT KIA VPL I QGY T VLR I L VEN RGRV NYGEN  
I DD QRK GLI GN LY L N D S PLK N FRI Y S L D M KKS FF QRF GLD KWX S L P E T P T L P A F F L G S L S I S  
S T P CDT FLK L E GWE KGV V FING QNL GRY WNI GP QK TLY L PGP WL S S G I N QV I V F E E T M A G P A  
L QFT E T P H L G R N QY I K

**Signal sequence:**

amino acids 1-27

**Casein kinase II phosphorylation site.**

amino acids 141-118, 253-257, 340-344, 395-399, 540-544, 560-564

**N-myristoylation site.**

amino acids 146-152, 236-242, 240-246, 244-250, 287-293, 309-315,  
320-326, 366-372, 423-429, 425-431, 441-447, 503-509, 580-586

## **FIGURE 65**

GGGGACGCGGAGCTGAGAGGCTCCGGCTAGCTAGGTAGGGGTGGACGGTCCAGGACC  
CTGGTGAGGGTTCTACTTGGCCTTCGGTGGGGTCAAGACGCAGGCACCTACGCCAAAGG  
GGAGCAAGCCGGCTCGGCCGAGGCCCCCAGGACCTCCATCTCCAAATGTTGGAGGAATC  
CGACACGTACGGTCTGTCCCGTCTCAGACTAGAGGAGCGCTGTAAACGCC**ATGGCTCCC**  
AAGAAGCTGCTCGCTTCGTTCTGCTGAGTGGATAGGGGTATGACCGGTTCTCCTAGACGGGGCC  
GGCAGACACTCGGTGTTCTGCTGAGTGGATAGGGGTATGACCGGTTCTCCTAGACGGGGCC  
CGTCCGCTATGTCTGGCAGCCTGCACTACTTCGGGTACCGCGGGTCTTGGGCCGAC  
CGGCTTTGAAGATGCGATGGAGCGGCCTCAAGCCATACAGTTATGTGCCCTGGAACTA  
CCACGAGCCACAGCCTGGGGTCTATAACTTAATGGCAGCCGGACCTCATTGCCCTTCTGA  
ATGAGGCAGCTCTAGCGAACCTGTTGGTCATACTGAGACCAGGACCTACATCTGTGCAGAG  
TGGGAGATGGGGGTCTCCCATCCTGGTCTCGAAAACCTGAAATTCTATCTAAGAACCTC  
AGATCCAGACCTCCTGCCGAGTGGACTCTGGTTCAAGGTCTGCTGCCCAAGATATATC  
CATGGCTTATCACAATGGGGCAACATCATTAGCATTAGGTGGAGAATGAATATGGTAGC  
TACAGAGCCTGTGACTTCAGCTACATGAGGCACTTGGCTGGCTCTCGTCACTGCTAGG  
AGAAAAGATCTGCTCTCACACAGATGGGCCTGAAGGACTCAAGTGTGGCTCCCTCCGGG  
GAECTATACCACTGTAGATTGGCCCAGCTGACAACATGACCAAAATCTTACCCCTGCTT  
CGGAAGTATGAACCCCATGGGCCATTGGTAAACACTCTGAGTACTACACAGGCTGGCTGGATT  
CTGGGCCAGAATCACTCCACACGGTCTGTGTCAAGCTGAACCAAAGGACTAGAGAACATGC  
TCAAGTTGGGAGCCAGTGTGAACATGTACATGTTCCATGGAGGTACCAACTTGGATATTGG  
AATGGTGCCGATAAGAAGGGACGCTCCTCCGATTACTACCAGCTATGACTATGATGCACC  
TATATCTGAAGCAGGGGACCCACACCTAACGCTTTGCTCTCGAGATGTCATCAGCAAGT  
TCCAGGAAGTCCCTTGGACCTTACCTCCCCGAGCCCCAAGATGATGCTTGGACCTGTG  
ACTCTGCACCTGGTGGCATTACTGGCTTCTAGACTTGCTTGGCCCCGTGGCCCAT  
TCATTCAATCTGCCAATGACCTTGAGGCTGTCAAGCAGGACCATGGCTCATGTTGTACC  
GAACCTATATGACCCATACCATTGGAGCCAACACCATTCTGGTGCCAAATAATGGAGTC  
CATGACCGTGCCTATGTGATGGATGGATGGGTCTCAGGGTGTGGAGCGAAATATGAG  
AGACAAACTATTTGACGGGAAACTGGGTCCAAACTGGATATCTTGGTGGAGAACATGG  
GGAGGCTCAGCTTGGTCTAACAGCAGTGAACCTAACGGCCTGTTGAAGCCACCAATTCTG  
GGCAAACAACTCCTACCCAGTGGATGATGTTCCCTCTGAAAATTGATAACCTGTGAAGTG  
GTGGTTCCCTCCAGTTGCCAAATGCCATATCCTCAAGCTCTTCTGGCCCCACATTCT  
ACTCCAAAACATTCCAATTGGCTCAGTTGGGACACATTCTATATCTACCTGGATGG  
ACCAAGGGCCAAGTCTGGATCAATGGTTAACCTGGCCGTACTGGACAAAGCAGGGCC  
ACAACAGACCCCTACGTGCCAAGATTCTGCTGTTCTAGGGAGCCCTAACAAAATA  
CATTGCTGGAACTAGAAGATGTACCTCTCCAGCCCCAAGTCCAATTGGATAAGCCTATC  
CTCAATAGCACTAGTACTTGCACAGGACACATCAATTCCCTTCAGCTGATACACTGAG  
TGCCTCTGAACCAATGGAGTTAAGTGGCACT**GA**AAAGGTAGGCCGGCATGGTGGCTCATGC  
CTGTAATCCCAGCAGTTGGGAGGCTGAGACGGGTGGATTACCTGAGGTCAGGACTTCAAGA  
CCAGCCTGGCAACATGGTAAACCCCGTCTCCACTAAAAATACAAAAATTAGCCGGCGTG  
ATGGTGGGCACCTCTAATCCCAGCTACTTGGGAGGCTGAGGGCAGGAGAATTGCTGAATCC  
AGGAGGCAGAGGTTGCAGTGAGTGGAGGTTGTACCACTGCACTCCAGCCTGGCTGACAGTGA  
GACACTCCATCTCAAAAAAAA

## **FIGURE 66**

MAPKKLSCLRSLLLPLSLTLLLPQADTRSFVVDRGHDRFLLDGAPFRYVSGSLHYFRVPRVL  
WADRLLKMRWSGLNAIQFYVPWNYHEPQPGVYNFNGSRDLIAFLNEAALANLLVILRPGPYI  
CAEWEMGGLPSWLLRKPEIHLRTSDPDFLAAVDSWFKVLLPKIYPWLYHNGGNISIQVENE  
YGSYRACDFSYMRHLAGLFRALLGEKILLFTTDGPEGLKGSLRGLYTTVDFGPADNMTKIF  
TLLRKYEPHGPLVNSEYYTGWLWQNHSTRVSATKGLENMLKLGASVNMYMFHGGTNF  
GYWNGADKKGRFLPITTSYDYDAPISEAGDPTPKLFALRDVISKFQEVPGLPPSPKML  
GPVTLHLVGHLLAFLDLLCPRGPIHSILPMTFEAVKQDHGFMLYRTYMHTIFEPTFWVPN  
NGVHDRAYVMVDGVFQGVVERNMRDKLFLTGKLGSKLDILVENMGRSLFGNSDFKGLLKP  
PILGQTILTQWMMFPLKIDNLVKWWFPLQLPKWPYPQAPSGPTFYSKTFPILGSVGDTFLYL  
PGWTKGQVWINGFNLGRYWTKQGPQQTLYVPRFLLFPRGALNKITLLELEDVPLQPQVQFLD  
KPILNSTSTLHRTHINSLSAADTLSASEPMELSGH

**Signal sequence:**

amino acids 1-27

**N-glycosylation site.**

amino acids 97-101, 243-247, 276-280, 486-490, 625-629

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 4-8

**Casein kinase II phosphorylation site.**

amino acids 148-152, 234-238, 327-331, 423-427, 469-473, 550-554,  
603-607, 644-648

**Tyrosine kinase phosphorylation site.**

amino acids 191-198

**N-myristoylation site.**

amino acids 131-137, 176-182, 188-194, 203-209, 223-229, 227-233,  
231-237, 274-280, 296-300, 307-313, 447-453, 484-490

## FIGURE 67

GCTTGAAACACGTCTGCAAGCCAAAGTTGAGCATCTGATTGGTTATGAGGTATTGAGTGC  
ACCCACAATATGGCTTACATGTTGAAAAAGCTTCTCATCAGTTACATATCCATTATTGTGT  
TTATGGTTTATCTGCCTCTACACTCTTCTGGTTATTCAAGGATACCTTGAGGAATATT  
CTTCGAAAAAGTCAGAGAAGAGAGCAGTTAGTGACATTCCAGATGTCAAAACGATTT  
GCGTCCTCTTCACATGGTAGACCAGTATGACCAGCTATATTCCAAGCGTTGGTGTGTT  
CTTGTCAAGTTAGTGAAAATAAACTTAGGAAATTAGTTGAACCATGAGTGGACATTG  
AAAAACTCAGGCAGCACATTCAACGCCAGGACAAGCAGGAGTTGCATCTGTTCATG  
CTGTCGGGGTGCCCGATGCTGTCTTGACCTCACAGACCTGGATGTGCTAAAGCTTGA  
AATTCCAGAAGCTAAAATTCTGCTAAGATTCTCAAATGACTAACCTCCAAGAGCTCCACC  
TCTGCCACTGCCCTGCAAAAGTTGAACAGACTGCTTTAGCTTCTCGCGATCACTGAGA  
TGCCTTCACGTGAAGTTCACTGATGTGGCTGAAATTCCCTGCCTGGGTGTATTGCTCA  
CCTTCGAGAGTTGTACTTAATAGGCAATTGAACTCTGAAAACAATAAGATGATAGGACTTG  
AATCTCTCCGAGAGTTGCGGCACCTTAAGATTCTCACGTGAAGAGCAATTGACCAAAGTT  
CCCTCCAACATTACAGATGTGGCTCCACATCTTACAAAGTTAGTCATTATAATGACGGCAC  
TAAACTCTGGTACTGAACAGCCTTAAGAAAATGATGAATGTCGCTGAGCTGGAACCTCCAGA  
ACTGTGAGCTAGAGAGAATCCCACATGCTATTTCAGCCTCTCTAATTACAGGAACGGAT  
TTAAAGTCCAATAACATTGCACAATTGAGGAAATCATCAGTTCCAGCATTAAAACGACT  
GACTTGTAAAATTATGGCATAACAAAATTGTTACTATTCCCTCCCTATTACCCATGTCA  
AAAACTTGGAGTCACTTATTCTCTAACACAAGCTCGAACCTTACAGTGGCAGTATT  
AGTTACAGAAAACTCAGATGCTTAGATGTGAGCTACAACAAACATTCAATGATTCCA  
AATAGGATTGCTTCAGAACCTGCAGCATTGCATATCACTGGAACAAAGTGGACATTCTGC  
CAAAACAATTGTTAAATGCATAAAAGTTGAGGACTTTGAATCTGGACAGAACTGCATCACC  
TCACTCCCAGAGAAAAGTTGGTCAGCTCTCCAGCTCACTCAGCTGGAGCTGAAGGGAACTG  
CTTGGACCGCCTGCCAGCCCAGCTGGCCAGTGTGGATGCTCAAGAAAAGCGGGTTGTTG  
TGGAAGATCACCTTTGATACCCGCCACTCGAACGTCAAAGAGGGATTGAATCAAGACATA  
AATATTCCCTTGCAAATGGATTTAAACTAAGATAATATGACAGTGATGTGCAGGAAC  
AACTCCTAGATTGCAAGTGCTCACGTACAAGTTATTACAAGATAATGCATTAGGAGTAG  
ATACATCTTTAAAATAAAACAGAGAGGATGCATAGAACGGCTGATAGAACAGACATAACTGA  
GTTCAATGTTGTAGGGTTTAAGTCATTCAATTCCAAATCATTGTTTTCTTTGGGG  
AAAGGGAAGGAAAATTATAATCACTAATCTGGTTCTTTAAATTGTTGTAACGGAT  
GCTGCCGCTACTGAATGTTACAAATTGCTTGCCCTGCTAAAGTAAATGATTAAATTGACATT  
TTCTTACTAAAAAAAAAAAAAA

## **FIGURE 68**

MAYMLKKLLISYISIICVYGFICLYTLFWLFRIPLKEYSFEKVREESSFSDIPDVKNDFAFL  
LHMVDQYDQLYSKRGVFLSEVSENKLREISLNHEWTFEKLQRQHISRNAQDKQELHLFMLSG  
VPDAVFDLTDLDVLKLELIPEAKIPAKISQMTNLQELHLCHCPAKVEQTAFSFLRDHLRCLH  
VKFTDVAEIPA WVYLLKNLRELYLIGNLNSENNK MIGLES LREL RHLKILHVKS NLTKVPSN  
ITDVAPH LTKLVIHNDGT KLLVLN S LKKMMNVAE LELQNCE LERI P HAI F SLSN LQEL DLKS  
NNIRTIEEIISFQHLKRLTCLKLWHNKIVTIPPSI THVKNLES LYFSNNKLES LPVAVFSLQ  
KLRCLDVSYNNISMIPIEIGLLQNLQHLHITGNKVDILPKQLFKCIKLRTLNLGQNCITS LP  
EKVGQLSQLTQLELKGNCLDR LPAQLGQCRMLKKSGL VVEDHLFDTLPLEVKEALNQDINIP  
FANGI

**Signal sequence:**

amino acids 1-20

**N-glycosylation site.**

amino acids 241-245, 248-252, 383-387

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 326-330

**Casein kinase II phosphorylation site.**

amino acids 48-52, 133-137, 226-230, 315-319, 432-436, 444-448

**Tyrosine kinase phosphorylation site.**

amino acids 349-355, 375-381

**N-myristoylation site.**

amino acids 78-84, 124-130, 212-218, 392-398

## **FIGURE 69**

CCACCGCGTCCGGCCTTCTCTGGACTTGCATTCCATTCTTTGACAAACTGACTTTTTATTC  
TTTTTCCATCTCTGGGCAGCTGGATCCTAGGCCCTGGAAAGACATTGTGTTACACACATAAGGAT  
CTGTGTTGGGTTCTTCTTCCCTCCCTGACATTGGCATTGCTTAGTGGTTGTGGGGAGGGACCGACGTGG  
GCTCAGTGCTTGCTGCACTTATCTGCCTAGGTACATCGAAGTCTTGACCTCCATACAGTGATTATGCCTGTC  
ATCGCTGGTGGTATCTGGCGGCTGCTCTGCTGATAGTTGTCGTCTGCTCTTACTCTAAAATACACAAAC  
GCGCTAAAAGCTGCAAAGGAACCTGAAAGCTGTTGCTGTAAAAATCACAAACCCAGACAAGGTGTGGTGGGCAAG  
AACAGCCAGGCCAAAACCATTGCCACGGAGCTGCTGCTGCGACATAATGAGGGCTCTGAGTTAGGAAAGGCTCCCTCTCAA  
AGTTTGATTCCCTGCCACCTGCTGCTGCGACATAATGAGGGCTCTGAGTTAGGAAAGGCTCCCTCTCAA  
GCAGAGCCCTGAAGACTTCAATGATGTCATGAGGCCACCTGTTGTGATGTCAGGCCACAGAAGAAAGGCCAG  
CTCCCCATCAGTTCATGAAAATAACTCAGTGCTGCTGGAAACAGCTGCTGGAGATCCCTACAGAGAGCTTC  
CACTGGGGCAACCTTCAGGAAGGAGTTGGGGAGAGAGAACCCACTGTTGGGAATGCTGATAAACCAGTTC  
CACAGCTGCTCTTCTCACACAAATCTACCCCTGCGTGGACTGACGTTCCCTGGAGGTGTCCAGAAA  
GCTGATGTAACACAGAGCTATAAAAGCTGTCGGCTTAAGGCTGCCAGGCCCTGCAAATGGAGCTTGT  
AGAAGGCTCATGCCATTGACCCCTTAATTCTCTGTTGGCGAGCTGACAATGGGGAGGCTGAAGGCAAT  
GCAAGCTGCACAGTCAGTCTAGGGGGTGCACATGGCAGAGACCCACAAGGCATGATCTGCAACTCAATCCC  
AGTGAGAACTGCACCTGGACAATAGAAAGACCAAGAAAACAAAGCATCAGAATTATCTTCTATGTCCAGCTT  
GATCCAGATGGAAGCTGTAAGGATGAAAACATTAAAGCTTTGACGGAACCTCCAGCAATGGGCCTGCTAGGG  
CAAGTCTGCAGAAAAAGACTATGTCCTGATTTGAATCATCAGTACATTGACGTTCAAATAGTTACT  
GAATCAGCAAGAATTCAAAGAACTGTCCTTGTCTTACTACTTCTCTCTAACATCTTCTATTCCAAACTGT  
GGCGGTTACCTGGATACCTTGGAAGGATCCTCACAGCCCAATTACCCAAAGCCGATCCTGAGCTGGCTTAT  
TGTGTTGGCACATACAAGTGGAGAAAGATTACAAGATAAAACTAACTCAAAGAGATTTCCTAGAAATAGAC  
AAACAGTGCAAATTGATTCTTCTGCCATCTATGATGGCCCTCACCACACTGCGCTGATTGGACAAGTCTGT  
GGCCGTGTGACTCCCACCTTCGAATCGTCATCAAACCTCTGACTGTCGTGTTGTCTACAGATTATGCCAATTCT  
TACCGGGGATTCTGCTTCTCACACCTCAATTATGCAGAAAACATCAACACTACATCTTAACTTGTCTTCT  
GACAGGATGAGAGTTATTATAAGCAAATCCTACCTAGAGGTTAACTCTAATGGGAATAACTTGTCAACTAAA  
GACCCAATTGCGAGACCAAAATTCAAATGTTGGAATTCTGTCCTCTTAATGGATGTTGACAATCAGA  
AAGGTTAGAAGATCAGTCATTACTTACACCAATAATCACCTTCTGTCATCCTCAACTTCTGAAAGTGATCACC  
CGTCAGAAACAACTCCAGATTATGTAAGTGTGAAATGGGACATAATTCTACAGTGGAGATAATATAACAA  
GAAGATGATGTAATACAAGTCAAATGCACTGGGAAATATAACACAGCATGGCTCTTTGAATCCAATTCA  
TTTGGAAAAGACTATACTGAAATCACCATATTATGTTGGAACCAACTCTTGTCAAGTTAGTCTGCAC  
ACCTCAGATCCAAATTGGTGGTTCTGATACCTGTAAGGTGATCCCTATTGGACACTATGGGAGA  
TACGACCTAATCAAGAGTGGATGTAAGTGTGAGATGAAACTTGTAAAGGTGATCCCTATTGGACACTATGGGAGA  
TTCCAGTTAATGCCCTTAAATTCTGAGAAGTATGAGCTGTGATCTGCACTGTAAGTTGTATATGTGAT  
AGCAGTGACCACCAGTCTGCTGCAATCAAGGTTGTGCTCCAGAAGCAAACGGAGACATTCTCATATAAATGG  
AAAACAGATTCCATCATAGGACCCATTGTCGAAAGGGATGAAAGTGCAGTGGCAATTCAAGGATTCAGGATTCAGCAT  
GAAACACATGCCAAGAAACTCCAAACCGCCCTTCAACAGTGTGCATCTGTTCTCATGGTTCTAGCTG  
AATGTGGTACTGTAGCGACAATCACAGTGAGGCATTGTAATCAACGGGAGACTACAAATACCAGAAGCTG  
CAGAACTATTAACTAACAGGTCCAACCTAAGTGAGACATGTTCTCCAGGATGCCAAAGGAAATGCTACCTCGT  
GGCTACACATATTGAATAATGAGGAAGGGCCTGAAAGTGACACACAGGCCCTGCATGAAAAAAA

## **FIGURE 70**

MELVRLMPPTLLILSCLAEATMAEAEGRASCTVSLGGANMAETHKAMILQLNPSENCTWTI  
ERPENKSIRIIIFSYVQLDPGSCESENIVFDGTSSNGPLLGQVCSKNDYVPVFESSSSTLT  
FQIVTDSARIQRTVFVFFSPNISIPNCGGYLDTLEGSFTSPNPKPHPELAYCVWHIQV  
EKDYKIKLNFKEIFLEIDKQCKFDLAIYDGPSNTSGLIGQVCRVTPTFESSNSLTVVLS  
TDYANSYRGFSASYTSIYAENINTTSLTCSRDRMVIISKSYLEAFNSNGNNLQLKDPTCRP  
KLSNVVEFSVPLNGCGTIRKVEDQSIYTNIITFSASSTSEVITRQKQLQIIVKCEMGHNST  
VEIIYITEDDVIQSQNALGKYNTSMALFESNSFEKTIILESPYYVDLNQTLFVQVSLHTSDPN  
LVVFLDTCRASPTDFASPTYDLIKSGCSRDETCKVYPLFGHYGRFQFNFKFLRSMSSVYL  
QCKVLICDSSDHQSRCNQGCVRSRDKDISSYKWKTDIIGPIRLKDRSASGNSGFQHETHA  
EETPNQPFNSVHLFSFMVLALNVVTVATITVRHFVNQRADYKYQKLQNY

**Signal sequence:**

amino acids 1-24

**Transmembrane domain:**

amino acids 571-586

**N-glycosylation site.**

amino acids 29-33, 57-61, 67-71, 148-152, 271-275, 370-374,  
394-398, 419-423

**Casein kinase II phosphorylation site.**

amino acids 22-26, 108-112, 289-293, 348-352, 371-375, 379-383,  
408-412, 463-467, 520-524, 556-560

**Tyrosine kinase phosphorylation site.**

amino acids 172-180, 407-415, 407-416, 519-528

**N-myristoylation site.**

amino acids 28-34, 38-44, 83-89, 95-101, 104-110, 226-232

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 7-18

## **FIGURE 71**

GACGGAAGAACAGCGCTCCCGAGGCCGCGGGAGCCTGCAGAGAGGACAGCCGGCCTGCGCCG  
GGACATGCGGCCCCAGGAGCTCCCAGGCTCGCGTTCCCGTTGCTGCTGTTGCTGC  
TGCTGCCGCCGCCGTGCCCTGCCACAGCGCCACGCCGCTCGACCCCACCTGGGAGTCC  
CTGGACGCCGCCAGCTGCCCGCGTGGTTGACCAGGCAAGTCGGCATCTTCATCCACTG  
GGGAGTGTTCGCCCAGCTCGTAGCGAGTGGTCTGGGGTATTGGCAAAGGAAA  
AGATACCGAAGTATGTGAATTATGAAAGATAATTACCCCTCTAGTTCAAATATGAAGAT  
TTGGACCACTATTACAGCAAATTAAAAATGCAACCAGTGGGAGATATTTCAGGC  
CTCTGGTGCAAATACATTGTCTTAACCTCAAACATCATGAAGGCTTACCTGTGGGGT  
CAGAATATTGTGGAACGTGGAATGCCATAGATGAGGGGCCAAGAGGGACATTGTCAAGGAA  
CTTGAGGTAGCCATTAGGAACAGAACTGACCTGCGTTGGACTGTACTATTCCCTTTGA  
ATGGTTCATCCGCTTCTGAGGATGAATCCAGTCATTCCATAAGCGGAATTCCAG  
TTTCTAAGACATTGCCAGAGCTATGAGTTAGTGAACAACATCAGCCTGAGGGTCTGTGG  
TCGGATGGTACGGAGGAGCACCGGATCAATACTGGAACAGCACAGGCTCTGGCCTGGTT  
ATATAATGAAAGCCCAGTCGGGGCACAGTAGTCACCAATGATCGTTGGGAGCTGGTAGCA  
TCTGTAAGCATGGTGGCTCTACCTGCAGTGATCGTTATAACCCAGGACATTTGCCA  
CATAAATGGAAAACATGCATGACAATAGACAAACTGTCCTGGGCTATAGGAGGAAGCTGG  
AATCTCTGACTATCTACAATTGAAGAATTGGTGAAGCAACTTGTAGAGACAGTTCATGTG  
GAGGAAATCTTGATGAATTGGGCCACACTAGATGGCACCATTTCTGTAGTTTGAG  
GAGCGACTGAGGCAAGTGGGCTCTGGCTAAAGTCATGGAGAAGCTATTATGAAACCTA  
TACCTGGCGATCCCAGAATGACACTGTCACCCAGATGTGTGGTACACATCCAAGCCTAAAG  
AAAAATTAGTCTATGCCATTCTAAATGGCCACATCAGGACAGCTGTTCTGGCCAT  
CCCAAAGCTATTCTGGGGCAACAGAGGTGAAACTACTGGCCATGGACAGCCACTTAAC  
GATTCTTGAGCAAATGGCATTATGGTAGAACTGCCACAGCTAACCATCAGATGC  
CGTGTAAATGGGCTGGCTAGCCCTAACTAATGTGATCTAAAGTGCAGCAGAGTGGCTG  
ATGCTGCAAGTTATGCTAAGGCTAGGAACATCAGGTGTCTATAATTGTAGCACATGGAGA  
AAGCAATGTAACGGATAAGAAAATTGGCAGTTCAGGCCCTTCCCTTTCCACTA  
AATTCTAAATTACCCATGTAACCATTAACTCTCCAGTGCACTTGCCATTAAAGTC  
TCTTCACATTGATTGTTCCATGTGTGACTCAGAGGTGAGAATTTCACATTATAGTAG  
CAAGGAATTGGTGGTATTATGGACCGAACTGAAAATTGTGAAGCCATATCCCCCATG  
ATTATATAGTTATGCATCACTTAATATGGGATATTCTGGAAATGCATTGCTAGTCAT  
TTTTTTGTGCCAACATCATAGAGTGTATTACAAAATCCTAGATGGCATAGCCTACTACA  
CACCTAATGTGTATGGTATAGACTGTTGCTCTAGGCTACAGACATATACAGCATGTTACTG  
AATACTGTAGGCAATAGTAACAGTGGTATTGTATATCGAAACATATGGAAACATAGAGAAG  
GTACAGTAAAATACTGAAAATAATGGTGCACCTGTATAGGGCACTTACCCAGGAATGGAG  
CTTACAGGACTGGAAGTTGCTCTGGGTGAGTCAGTGAGTGAATGTGAAGGCCTAGGACATTA  
TTGAACACTGCCAGACGTTATAAAACTGTATGCTTAGGCTACACTACATTATAAAAAAA  
GTTTTCTTCTTCATTATAAAACATAAGTGTACTGTAACTTACAAACGTTAAATT  
TTTAAACCTTTGGCTTTGTAATAACACTTAGCTAAAACATAAAACTCATTGTGCAA  
ATGTAA

## **FIGURE 72**

MRPQELPRLAFPLLLLLLPPPPCPAHSATRFDPTWESLDARQLPAWFDQAKFGIFIFIHWG  
VFSVPSFGSEWFWWYQKEKIPKYVEFMKDNYPPSFKYEDFGPLFTAKFFNANQWADIFQAS  
GAKYIVLTSKHHEGFTLWGSEYSWNNAIDEGPKRDIVKELEVAIRNRTDLRGFLYYSLFEW  
FHPLFLEDESSSFHKRQFPVSKTLPELYELVNYYQPEVLWSDGDGGAPDQYWNSTGFLAWLY  
NESPVRGTVVTNDRWGAGSICKHGGFYTCSDRYNPGHLLPHKWENCMTIDKLSWGYRREAGI  
SDYLTIEELVKQLVETVSCGGNLLMNIGPTLDGTISVVFEERLRQVGSWLKVNGEAIYETY  
WRSQNDTVTPDVWYTSKPKEKLVYAIFLKWPTSGQLFLGHPKAILGATEVKLLGHGQPLNWI  
SLEQNGIMVELPQLTIHQMPCKWGWALALTNVI

**Signal sequence:**

amino acids 1-28

**N-glycosylation site.**

amino acids 171-175, 239-243, 377-381

**Casein kinase II phosphorylation site.**

amino acids 32-36, 182-186, 209-213, 227-231, 276-280, 315-319,  
375-375

**Tyrosine kinase phosphorylation site.**

amino acids 361-369, 389-397

**N-myristoylation site.**

amino acids 143-149, 178-184, 255-261, 272-278, 428-434

**Leucine zipper pattern.**

amino acids 410-432

**Alpha-L-fucosidase putative active site.**

amino acids 283-295

## FIGURE 73

AGCAGGGAAATCCGGATGTCTCGGTTATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATAGT  
TCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAAGTGGCCATC  
TGAGGTGTTCCCTGGCTCTGAAGGGGTAGGCACGATGCCAGGTGCTTCAGCCTGGTGTG  
CTTCTCACTCCATCTGGACCACGAGGCTCCTGGTCCAAGGCTTTGCGTGCAGAAGAGCT  
TTCCATCCAGGTGTCAAGAATTATGGGGATCACCCCTGTGAGCAAAAGGCGAACCGC  
AGCTGAATTTCACAGAAGCTAAGGAGGCCTGTAGGCTGCTGGACTAAGTTGGCCGGCAAG  
GACCAAGTTGAAACAGCCTTGAAAGCTAGCTTGAACACTTGCAAGCTATGGCTGGGTTGGAGA  
TGGATTCGTGGTCATCTCTAGGATTAGCCAAACCCAAAGTGTGGAAAAATGGGGTGGGTG  
TCCTGATTGGAAGGTTCCAGTGAGCCGACAGTTGCAGCCTATTGTTACAACATCTGAT  
ACTTGGACTAACTCGTCATTCCAGAAATTATCACCAACAAAGATCCCATTCAACACTCA  
AACTGCAACACAAACAAACAGAATTATTGTCAAGTACACTCGTGGCATCCCC  
ACTCTACAATACCTGCCCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGG  
AGAAAAAAATTGATTGTGTCAAGAAGTTTATGGAAACTAGCACCATGTCTACAGAAAC  
TGAACCATTGTTGAAAATAAGCAGCATTCAAGAATGAAGCTGCTGGGTTGGAGGTGTCC  
CCACGGCTCTGCTAGTGCTCTCCTCTTGGTGTGCAGCTGGCTTGGAATTTGC  
TATGTCAAAAGGTATGTGAAGGCCTTCCCTTACAAACAAGAATCAGCAGAAGGAAATGAT  
CGAAACCAAAGTAGTAAAGGAGGAGAAGGCCAATGATAGCAACCTAATGAGGAATCAAAGA  
AAACTGATAAAACCCAGAAGAGTCCAAGAGTCCAAGCAAAACTACCGTGGATGCCTGGAA  
GCTGAAGTTAGATGAGACAGAAATGAGGAGACACACCTGAGGCTGGTTCTTCATGCTCC  
TTACCCCTGCCCGAGCTGGGAAATCAAAGGCCAAAGAACCAAGAACAGAAAGTCCACCC  
GGTTCTTAACGGAAATCAGCTCAGGACTGCCATTGGACTATGGAGTGCACCAAGAGAACATGC  
CCTTCTCCTTATTGTAACCTGTCTGGATCCTATCCTCCTACCTCCAAAGCTTCCCACGGCC  
TTTCTAGCCTGGCTATGTCCTAATAATATCCCACGGAGAAAGGAGTTTGCAAAGTGCAA  
GGACCTAAACATCTCATCAGTATCCAGTGGTAAAAGGCCCTGGCTGTCTGAGGCTAGG  
TGGGTTGAAAGCCAAGGAGTCACTGAGACCAAGGCTTCTACTGATTCCAGCTCAGAC  
CCTTCTCAGCTCTGAAAGAGAACACGTATCCACCTGACATGTCCTCTGAGCCGGTA  
AGAGCAAAAGAACATGGCAGAAAGTTAGCCCTGAAAGCCATGGAGATTCTCATAACTTGAG  
ACCTAATCTCTGTAAGCTAAAATAAGAACATAGAACAAAGGCTGAGGATAACGACAGTACACT  
GTCAGCAGGGACTGTAACACAGACAGGGTCAAAGTGTCTCTGAACACATTGAGTTGGA  
ATCACTGTTAGAACACACACACTTACTTTCTGGTCTCTACCACTGCTGATATTTCT  
AGGAAATATACTTTACAAGTAACAAAATAAAACTCTTATAAATTCTATTTTATCTGA  
GTTACAGAAATGATTACTAAGGAAGATTACTCACTAATTGTTAAAAAGTAATAAAATTCA  
ACAAACATTGCTGAATAGCTACTATATGTCAGTGCTGCAAGGTATTACACTCTGTAAT  
TGAATATTATCCTCAAAAATTGCACATAGTAGAACGCTATCTGGGAAGCTATTTTTCA  
GTTTGATATTCTAGCTTATCTACTTCCAAACTAATTCTATTTGCTGAGACTAATCTT  
ATTCACTTCTCTAATATGGCAACCATTATAACCTTAATTATTAAACATACCTAACAG  
TACATTGTTACCTCTATATACCAAGCACATTAAAGTGCCTTAACAAATGTATCACTA  
GCCCTCCTTTCCAACAAGAAGGGACTGAGAGATGCAGAAATATTGTGACAAAAATTAA  
AGCATTAGAAAATT

## **FIGURE 74**

MARCFSLVLLLTSIWTTRLLVQ GSLRAEELSIQVSCRIMGITLVS KANQQLNFTEAKEACR  
LLGLSLAGKDQVETALKASFETCSYGVGDGFVVISRISP NPKCGKNGVGVLIW KVPVSRQF  
AAYCYNSSDTWTNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYVASPYSTI PAPTTTPP  
APASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKA AFKNEAAGFGGVPTALLVLALLFF  
GAAAGLGFCYVKRYVKA FPTNKNQQKEMIETKVVKEEKANDSNPNEESKKTDKNPEESKSP  
SKTTVRCLEAEV

**Signal sequence:**

amino acids 1-16

**Transmembrane domain:**

amino acids 235-254

**N-glycosylation site.**

amino acids 53-57, 130-134, 289-293

**Casein kinase II phosphorylation site.**

amino acids 145-149, 214-218

**Tyrosine kinase phosphorylation site.**

amino acids 79-88

**N-myristoylation site.**

amino acids 23-29, 65-71, 234-240, 235-239, 249-255, 253-259

## **FIGURE 75**

AGATGGCGGTCTTGGCACCTCTAATTGCTCTCGTATTCGGTGCCGACTTTCACGATGG  
CTCGCCCAACCTTACTACCTCTGT~~CGGCC~~CTGCTCTGCTGCCTCCTACTCGTGAGGAA  
ACTGCCGCCCTGCCACGGTCTGCCACCCAAACGCGAAGACGGTAACCGTGTGACTTG  
ACTGGAGAGAAGTGGAGATCCTGATGTTCTCAGTGCCATTGTGATGATGAAGAACCGCAGA  
TCCATCACTGTGGAGCAACATATAGGCAACATTTCATGTTAGTAAAGTGGCAACACAAT  
TCTTTCTTCCGCTTGGATATTGCATGGCCTACTTACATCACACTCTGCATAGTGTCC  
TGATGACGTGCAAACCCCCCTATATATGGGCCCTGAGTATATCAAGTACTTCAATGATAAA  
ACCATTGATGAGGA~~ACTAGAACGGACAAGAGGGTC~~ACTTGGATTGTGGAGTTCTTGCAA  
TTGGTCTAATGACTGCCAATCATTGCCCTATCTATGCTGACCTCTCCCTAAATACAAC  
GTACAGGGCTAAATTTGGGAAGGTGGATGTTGGACGCTACTGATGTTAGTACGGTAC  
AAAGTGAGCACATCACCCCTACCAAGCAACTCCCTACCCTGATCCTGTTCCAAGGTGGCAA  
GGAGGCAATGCGCGGCCACAGATTGACAAGAAAGGACGGCTGTCTCATGGACCTCTCG  
AGGAGAATGTGATCCGAGAATTAACTTAAATGAGCTATACCAGCGGCCAAGAAACTATCA  
AAGGCTGGAGACAATATCCCTGAGGAGCAGCCTGTTCAACCCCCACCACAGTGTCA  
TGGGAAAACAAGAAGGATAAAATAGATCCTCACTTGGCAGTGCTCCTCTCGTCAATT  
CCAGGCTTTCCATAACCACAAGCCTGAGGCTGCAGCCTTNATTNATGTTCCCTTGG  
CTGNGACTGGNTGGGCAGCATGCAGCTCTGATTAAAGAGGCATCTAGGAATTGTCAG  
GCACCCCTACAGGAAGGCCTGCCATGCTGTGGCCA~~ACTGTTCA~~CTGGAGCAAGAAAGAGATC  
TCATAGGACGGAGGGGGAAATGGTTCCCTCAAGCTTGGTCAGTGTGTTACTGCTTATC  
AGCTATT~~CAGACATCTCCATGGTTCTCCATGAAACTCTGTGGTTCATCATT~~CCCTTTAG  
TTGACCTGCACAGCTGGTAGACCTAGATTAAACCTAAGGTAAGATGCTGGGTATAGAA  
CGCTAAGAATTTC~~CCCCAAGGACTCTGCTTCAAGCCCTCTGGCTCGTTATGGTC~~  
TTCATTAAAAGTATAAGCCTAAC~~TTGTCGCTAGCCTAAGGAGAAACCTTAACCACAAAG~~  
TTTTTATCATTGAAGACAATATTGAACAACCCCTATTGTGGGATTGAGAAGGGGTGAA  
TAGAGGCTTGAGACTTCC~~TTGTGGTAGGACTTGGAGAGAAATCCCTGGACTTCAC~~  
TAACCCCTGACATACTCCCCACACCAGTTGATGGCTTCCGTAATAAAAGATTGGGATT  
TCCTTTG

## **FIGURE 76**

MAVLAPLIALVYSVPRLSRWLAQPYYLLSALLSAAFLLVRKLPPPLCHGLPTQREDGNPCDFD  
WREVEILMFLSAIVMMKNRRSITVEQHIGNIFMFSKVANTILFFRLDIRMGLLYITLCIVFL  
MTCKPPLYMGPEYIKYFNDKTIDEELERDKRVTWIVEFFFANWSNDCQSFAPIYADLSLKYNC  
TGLNFGKVDVGRYTDVSTRYKVSTSPLTKQLPTLILFQGGKEAMRRPQIDKKGRAVSWTFSE  
ENVIREFNLNELYQRAKKLSKAGDNIPEEQPVASTPTTVSDGENKKDK

**Signal sequence:**

amino acids 1-48

**Transmembrane domain:**

amino acids 111-125

**N-glycosylation site.**

amino acids 165-169, 185-189

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 154-158, 265-269

**Casein kinase II phosphorylation site.**

amino acids 51-55, 145-149, 245-249, 286-290, 288-292

**N-myristoylation site.**

amino acids 188-194, 225-231

**Myb DNA-binding domain repeat signature 1.**

amino acids 244-253

## FIGURE 77

GGACAGCTCGCGCCCCGAGAGCTCTAGCCGTCGAGGAGCTGCCCTGGGACGTTGCCCTG  
GGGCCCCAGCCTGGCCCGGGTCACCCCTGGCATGAGGAGAGGGGCTGTTGCTCCTGGTCCA  
TTGCTCCTGCTGCCCGCTCCTACGGACTGCCCTCTACAACGGCTTCTACTACTCCAACAG  
CGCCAACGACCAGAACCTAGGCAACGGTCATGGCAAAGACCTCCTTAATGGAGTGAAGCTGG  
TGGTGGAGACACCCGAGGAGACCCTGTTCACCTACCAAGGGGCCAGTGTGATCCTGCCCTGC  
CGCTACCGCTACGAGCCGGCCCTGGTCTCCCCGGCGGTGTGCGTGTCAAATGGTGGAAAGCT  
GTCGGAGAACGGGCCAGAGAACGGACGTGCTGGTGGCCATCGGGCTGAGGCACCGCTCCT  
TTGGGACTACCAAGGCCGCGTGCACCTGCGGCAGGACAAAGAGCATGACGTCTCGCTGGAG  
ATCCAGGATCTGCGGCTGGAGGACTATGGCGTTACCGCTGTGAGGTATTGACGGCTGGA  
GGATGAAAGCGGTCTGGTGGAGCTGGAGCTGGGGGTGTGGCTTTCTTACCAAGTCCCCA  
ACGGCGCTACCAGTTCAACTTCCACCGAGGGCCAGCAGGTCTGTGAGACAGCAGGCTGCGGTG  
GTGGCCTCTTGAGCAGCTTCCGGGCTGGGAGGAGGGCCTGGACTGGTGCAACGCGGG  
CTGGCTGCAGGATGCTACGGTGCAGTACCCCATCATGTTGCCCGGCAGCCCTGCGGTGGCC  
CAGGCCTGGCACCTGGCGTGCAGCTACGGCCCCGCCACCGCCGCTGCACCGCTATGAT  
GTATTCTGCTTCGCTACTGCCCTCAAGGGCGGGTGTACTACCTGGAGCACCCCTGAGAAGCT  
GACGCTGACAGAGGCAAGGGAGGCCTGCCAGGAAGATGATGCCACGATGCCAAGGTGGAC  
AGCTTTGCCGCTGGAAAGTTCCATGGCTGGACCGCTGCGACGCTGGCTGGCTGGCAGAT  
GGCAGCGTCCGCTACCCCTGTGGTTACCCGCATCTTAACGTGGGCCCCAGAGCCTGGG  
CCGAAGCTTGGCTCCCCGACCCGCAGAGCCGTTGTACGGTGTACTGCTACCGCCAGC  
ACTAGGACCTGGGCCCTCCCTGCCGATTCCCTCACTGGCTGTATTATTGAGTGGTT  
CGTTTCCCTGTGGTTGGAGCCATTAACTGTTTATACTTCTCAATTAAATTCT  
TTAACATTTTTACTATTTTGTAAGCAAACAGAACCCAAATGCCCTCCCTTGCTCCTG  
GATGCCCACTCCAGGAATCATGCTTGCTCCCTGGGCATTGCGGTTTGCTGGCTTCTG  
GAGGGTTCCCCGCCATCCAGGCTGGCTCCCTCCCTTAAGGAGGTTGGTGGCCAGAGTGGG  
GGTGGCCTGTCTAGAATGCCGCCGGAGTCCGGGCATGGTGGGCACAGTTCTCCCTGCC  
CAGCCTGGGGGAAGAACGGGCCCTGGGGCTCCGGAGCTGGCTTGGCCTCTCCTGCC  
CACCTCTACTCTCTGTGAAGCCGCTGACCCAGTCTGCCACTGAGGGCTAGGGCTGGAA  
GCCAGTTCTAGGCTTCCAGGCAGAACATGAGGGAAAGAACACTCCCTCCCCGTTCC  
TCCCTCTCGGTTCAAAGAACATGTTGTCATTGTTCTCCTGTTCCCTGTGTGG  
GGAGGGGCCCTCAGGTGTGTACTTGGACAATAATGGTGCTATGACTGCCCTGGCAA  
AA  
AA

## **FIGURE 78**

MGLLLVPLLLPGSYGLPYNGFYYNSANDQNLGNHGKDLLNGVKLVVETPEETLFTYQ  
GASVILPCRYRYEPALVSPRRVRVKWWKLSENGAPEKDVLAIGLRHRSFGDYQGRVHLRQD  
KEHDVSLEIQDLRLEDYGRYRCEVIDGLEDESGLVELELRGVVFPYQSPNGRYQFNFHEGQQ  
VCAEQAAVVASFEQLFRAWEELDWCNAGWLQDATVQYPIMLPRQPCGGPGLAPGVRSYGR  
HRRLHRYDVFCFATALKGRVYYLEHPEKLTLTEAREACQEDDATIAKVGQLFAAWKFHGLDR  
CDAGWLADGSVRYPVVHPHPNCGPPEPGVRSFGFPDPQSRLYGVYCYRQH

**Signal sequence:**

amino acids 1-17

**Casein kinase II phosphorylation site.**

amino acids 29-33, 53-57, 111-115, 278-282

**Tyrosine kinase phosphorylation site.**

amino acids 137-145

**N-myristoylation site.**

amino acids 36-42, 184-190, 208-214, 237-243, 297-303, 307-313

## **FIGURE 79**

GGAGAGCGGAGCGAAGCTGGATAACAGGGGACCG**TG**ATGTGGCACCACAGTTCTGCTGC  
TTCTGTTGCTACTGAGGCACGGGGCCAGGGGAAGCCATCCCCAGACGCAGGCCCTCATGGC  
CAGGGGAGGGTGCACCAGGCGCCCCCTGAGCGACGCTCCCCATGATGACGCCACGGGAA  
CTTCCAGTACGACCATGAGGCTTCCTGGACGGGAAGTGGCAAGGAATTGACCAACTCA  
CCCCAGAGGAAAGCCAGGCCGTCTGGGCGGATCGTGGACCGCATGGACCGCGGGGGAC  
GGCGACGGCTGGGTGCGCTGGCCGAGCTCGCGCGTGGATCGCGCACACGCAGCAGCGCA  
CATACGGACTCGGTGAGCGCGCCTGGACACGTACGACACGGACCGCGACGGCGTGTGG  
GTTGGGAGGAGCTGCGCAACGCCACCTATGCCACTACGCGCCCGTGAAGAATTGAC  
GTGGAGGATGCAGAGACCTACAAAAAGATGCTGGCTGGACGAGCGCGTTCCGGGTGGC  
CGACCAGGATGGGACTCGATGCCACTCGAGAGGAGCTGACAGCCTTCCTGCACCCCGAGG  
AGTCCCTCACATGCGGACATCGTATTGCTGAAACCCCTGGAGGACCTGGACAGAAACAAA  
GATGGCTATGTCCAGGTGGAGGAGTACATCGCGATCTGTACTCAGCCAGCCTGGGGAGGA  
GGAGCCGGCGTGGTGCAGACGGAGAGGCAGCAGTCCGGACTTCCGGATCTGAACAAGG  
ATGGGCACCTGGATGGAGTGAGGTGGCCACTGGTGCTGCCCTGCCAGGACCGCC  
CTGGTGGAAAGCCAACCACCTGCTGCACGAGAGCGACACGGACAAGGATGGCGCTGAGCAA  
AGCGGAAATCCTGGTAATTGAAACATGTTGTGGCAGTCAGGCCACCAACTATGGCGAGG  
ACCTGACCCGGCACACGATGAGCT**TG**AGCACCGCGACCTGCCACAGCCTCAGAGGCCG  
CACAAATGACCGGAGGAGGGCCGCTGGTCTGGCCCTCCCTGTCCAGGCCCGCAGGAG  
GCAGATGCAGTCCAGGCATCCTCCTGCCCTGGCTCTCAGGGACCCCTGGTCGGCTTC  
TGTCCCTGTCACACCCCAACCCAGGGAGGGCTGTCATAGTCCCAGAGGATAAGCAATAC  
CTATTCTGACTGAGTCTCCAGCCCAGACCCAGGGACCCCTGGCCCAAGCTCAGCTCTAA  
GAACCGCCCCAACCCCTCCAGCTCAAATCTGAGCCTCCACCATAGACTGAAACTCCCT  
GGCCCCAGCCCTCTCCTGCCTGGCCTGGACACCTCCTCTGCCAGGAGGAATAA  
AAGCCAGCGCCGGGACCTTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAA

## **FIGURE 80**

MMWRPSVLLLLLRLHGAQGKPSPDAGPHQGRVHQAAPLSDAPHDDAHGNFQYDHEAFLGR  
EVAKEFDQLTPEESQARLGRIVDRMDRAGDGWVSLAELRAWIAHTQQRHIRDSVSAAWDT  
YDTDGRVGWEELRNATYGHYAPGEFHDVEDAETYKKMLARDERRFRVADQDGDSMATRE  
ELTAFLHPEEFPHMRDIVIAETLEDLDRNKDGYVQVEEYIADLYSAEPGEEEPAWVQTERQQ  
FRDFRDLNKGHDGSEVGHVLPPAQDQPLVEANHLLHESDTDKDGRLSKAEILGNWNMFV  
GSQATNYGEDLTRHHDEL

**Signal sequence:**

amino acids 1-20

**N-glycosylation site.**

amino acids 140-144

**Casein kinase II phosphorylation site.**

amino acids 72-76, 98-102, 127-131, 184-188, 208-212, 289-293,  
291-295, 298-302

**N-myristoylation site.**

amino acids 263-269, 311-317

**Endoplasmic reticulum targeting sequence.**

amino acids 325-330

## **FIGURE 81**

GGGGCCTTGCCTCCGCACTCGGGCGCAGCCGGGTGGATCTCGAGCAGGTGC GGAGCCCCGG  
GCGGCAGGGCGCGGGTGCAGGGGATCCCTGACGCCCTCTGTCCTGTTCTTGTGCTCCCAG  
CCTGTCTGTCGTCTTGGCGCCCCGCTCCCCGCGGTGCGGGGTTGCACACCGATCCTG  
GGCTTCGCTCGATTGCCCGAGGGCGCTCCCAGACCTAGAGGGGGCTGGCCTGGAGCAG  
CGGGTCGTCTGTCCTCTCCCTGCGCCGCCCCGGGATCCGAAGGGTGC GGGGCTCT  
GAGGAGGTGACGCGGGGCTCCCGCACCTGGCCTGCCCCTGCATTCTCCCTCTCCCAG  
GTGTGAGCAGCCTATCAGTCACCATGTCCGCAGCCTGGATCCC GGCTCTGGCCTCGGTGTG  
TGTCTGCTGCTGCTGCCGGGCCCCGGGCAGCGAGGGAGCCGCTCCCATTGCTATCACATG  
TTTACACAGGGCTTGGACATCAGGAAAGAGAAAGCAGATGTCCTCTGCCAGGGGCTGCC  
CTCTTGAGGAATTCTCTGTGTATGGGAACATAGTATATGCTTCTGTATCGAGCATATGTGGG  
GCTGCTGTCCACAGGGGAGTAATCAGCAACTCAGGGGACCTGTACGAGTCTATAGCCTACC  
TGGTCGAGAAAACATTCCCTCAGTAGATGCCAATGGCATCCAGTCTCAAATGCTTCTAGAT  
GGTCTGCTCTTCACAGTAACAAAGGCAAAGTAGTACACAGGAGGCCACAGGACAAGCA  
GTGTCCACAGCACATCCACCAACAGGTAAACGACTAAAGAAAACACCCGAGAAGAAAACGG  
CAATAAAGATTGTAAGCAGACATTGCATTCTGATTGATGGAAGCTTAATATTGGCAGC  
GCCGATTAAATTACAGAAGAATTGGAAAGTGGCTCTAATGTTGGAAATTGGAAACA  
GAAGGACCACATGTGGCCTTGTCAAGCCAGTGAACATCCAAAATAGAATTACTTGAA  
AAACTTACATCAGCCAAAGATGTTGTTGCCATAAAGGAAGTAGGTTCAGAGGGGTA  
ATTCCAATACAGGAAAAGCCTGAAGCATACTGCTCAGAAATTCTCACGGTAGATGCTGGA  
GTAAGAAAAGGGATCCCCAAAGTGGTGGTATTATTGATGTTGGCCTCTGATGACAT  
CGAGGAAGCAGGCATTGTGGCAGAGAGTTGGTGTCAATGTATTATAGTTCTGTGGCCA  
AGCCTATCCCTGAAGAACTGGGATGGTCAGGATGTCACATTGTTGACAAGGCTGTCTG  
CGGAATAATGGCTTCTCTTACACATGCCCAACTGGTTGGCACCAAAATACGTAAA  
GCCTCTGGTACAGAACGCTGTGCACTCATGAACAAATGATGTCAGCAAGACCTGTTATAACT  
CAGTGAACATTGCCCTTCTAATTGATGGCTCCAGCAGTGTGGAGATAGCAATTCCGCC  
ATGCTTGAATTGTTCCAACATAGCCAAGACTTTGAAATCTGGACATTGGTCCAAGAT  
AGCTGCTGTACAGTTACTTATGATCAGCGCACGGAGTTCACTGACTATAGCACCA  
AAGAGAATGTCCTAGCTGTCACTAGAAACATCCGCTATATGAGTGGTGGAACAGCTACTGG  
GATGCCATTCTCACTGTTAGAAATGTGTTGGCCCTATAAGGGAGAGCCCCAACAGAA  
CTTCCTAGTAATTGTCACAGATGGGCAGTCCTATGATGATGTCAGGCCCCCTGCAGCTGCTG  
CACATGATGCAGGAATCACTATCTCTGTGGTGTGGCTGGCACCTCTGGATGACCTG  
AAAGATATGGCTTCTAAACCGAAGGAGTCTCAGGTTCTTACAAGAGAGTTCACAGGATT  
AGAACCAATTGTTCTGATGTCATCAGAGGCATTGAGAGATTCTTAGAATCCCAGCAAT  
AAGGTAACATTGACAACAGAAAGAAAAGTACAAGGGGATCCAGTGTGTAATTGTATT  
CTCATAATACTGAAATGCTTACTGATGAAATCAGATAACAAACTATTAAGTATGTCAAC  
AGCCATTAGGCAAATAAGCACTCCTTAAAGCCGCTGCCTCTGGTTACAATTACAGTGT  
ACTTTGTTAAAACACTGCTGAGGCTTCATAATCATGGCTCTTAGAAAACCTCAGGAAAGAGGA  
GATAATGTGGATTAAAACCTTAAGAGTTCTAACCATGCCTACTAAATGTACAGATATGCAAA  
TTCCATAGCTCAATAAAAGAATCTGATACTTAGACCAAAAAAAA

## FIGURE 82

MSAAWIPALGLGVCLLLLPGPAGSEGAAPIAITCFTRGLDIRKEKADVLCPGGCPLEFSVY  
GNIVYASVSSICGAAVHRGVISNSGGPVRVYSLPGRENYSSVDANGIQSQMLSRWSASFTVT  
KGKSSTQEATGQAVSTAHPPTGKRLKKTPPEKKTGNKDCCKADIAFLIDGSFNIQORRFNLQKN  
FVGKVALMLGIGTEGPHVGLVQASEHPKIEFYLKNFTSAKDVLFAIKEVGFRGGNSNTGKAL  
KHTAQKFFTVDAGVRKGIPKVVVVFIDGWPSSDIEEAGIVAREFGVNVFIVSVAKPIPEELG  
MVQDVTFVDKAVCRNNNGFFSYHMPNWFGTTKYVKPLVQKLCTHEQMMCSKTCYNSVNIAFLI  
DGSSSVGDSNFRMLFEVSNIAKTFEISDIGAKIAAVQFTYDQRTESFTDYSTKENVLAVI  
RNIRYMSGGTATGDAISFTVRNVFGPIRESPNKNFLVIVTDGQSYDDVQGPAAAHDAGITI  
FSVGVAWAPLDDLKDMASKPKESHAFFTREFTGLEPIVSDVIRGICRDFLESQQ

**Signal sequence:**

amino acids 1-24

**N-glycosylation site.**

amino acids 100-104, 221-225

**Casein kinase II phosphorylation site.**

amino acids 102-106, 129-133, 224-228, 316-320, 377-381, 420-424,  
425-429, 478-482, 528-532

**N-myristoylation site.**

amino acids 10-16, 23-29, 81-87, 135-141, 158-164, 205-211,  
239-245, 240-246, 261-267, 403-409, 442-448, 443-449

**Amidation site.**

amino acids 145-149

## FIGURE 83

CGCCCGCGCTCCCGCACCGCGGGCCCGCCACCGCGCCGCTCCGCATCTGCACCCGCAGCCC  
GGCGGCCTCCGGCGGGAGCGAGCAGATCCAGTCCGGCCCGCAGCGCAACTCGGTCCAGTCG  
GGCGCGGGCTGCGGGCGCAGAGCGAGAT**GCAGCGGCTTGGGCCACCC**TGCTGTGCCCTGC  
TGCTGGCGGGCGGGTCCCCACGGCCCCCGCGCCGCTCCGACGGCGACCTCGGCTCCAGTC  
AAGCCCGGCCGGCTCTCAGCTACCCGAGGAGGAGGCCACCCCAATGAGATGTTCCGCGA  
GGTGAGGAACGTATGGAGGACACGCAGCACAAATTGCGCAGCGCGGTGGAAGAGATGGAGG  
CAGAAGAAGCTGCTGCTAAAGCATCATCAGAAGTGAACCTGGCAAACACTACCTCCAGCTAT  
CACAATGAGACCAACACAGACACGAAGGTTGAAATAATACCATCCATGTGCACCGAGAAAT  
TCACAAGATAACCAACAACCAGACTGGACAAATGGTCTTTCAGAGACAGTTATCACATCTG  
TGGGAGACGAAGAAGGCAGAAGGAGCCACGAGTGCATCATCGACGAGGACTGTGGGCCAGC  
ATGTA  
CTGCACCCGGGACAGTGAGTGCTGTGGAGACCAGCTGTGTCTGGGTCACTGCACCAAAA  
TGGCCACCAGGGGAGCAATGGGACCATCTGTGACAACCAGAGGGACTGCCAGCCGGGCTG  
TGCTGTGCCTCCAGAGAGGGCTGCTGTTCCCTGTGTGCACACCCCTGCCGTGGAGGGCGA  
GCTTGCCATGACCCGCCAGCGGCTTCTGGACCTCATCACCTGGAGCTAGAGCCTGATG  
GAGCCTGGACCGATGCCCTGTGCCAGTGGCCTCCTCTGCCAGCCCCACAGCCACAGCCTG  
GTGTATGTGTGCAAGCCACCTCGTGGGGAGCCGTGACCAAGATGGGGAGATCCTGCTGCC  
CAGAGAGGTCCCCGATGAGTATGAAGTTGCCAGCTTCATGGAGGAGGTGCCAGGGAGCTGG  
AGGACCTGGAGAGGAGCCTGACTGAAGAGATGGCGCTGGGGAGCCTGCCGTGCCGCT  
GCACTGCTGGAGGGAGAGATT**TAG**ATCTGGACCAGGCTGTGGTAGATGTGCAATAGAA  
ATAGCTAATTATTCCCCAGGTGTGCTTAGGCGTGGCTGACCAGGCTTCTCCTACA  
TCTTCTTCCCAGTAAGTTCCCTCTGGCTTGACAGCATGAGGTGTTGTCATTGTTCA  
TCCCCCAGGCTGTTCTCCAGGCTTCACAGTCTGGTGTGCTGGAGAGTCAGGCAGGGTTAAC  
TGCAGGAGCAGTTGCCACCCCTGTCCAGATTATTGGCTGCTTGCCTCTACAGTTGGCAG  
ACAGCCGTTGTTCTACATGGCTTGATAATTGTTGAGGGAGGAGATGGAAACAATGTGG  
AGTCTCCCTGATTGGTTGGGAAATGTGGAGAAGAGTCAGGCCTGCTTGCAAAACATCAA  
CCTGGCAAAATGCAACAAATGAATTTCACCGCAGTTCTTCCATGGCATAGGTAAGCTG  
TGCCTTCAGCTGTTGCAAGATGAAATGTTCTGTTCAACCTGCATTACATGTGTTATT  
CATCCAGCAGTGTGCTCAGCTCCTACCTCTGCCCCAGCATTTCATATCCAAGATCAATT  
CCTCTCTCAGCACAGCCTGGGGAGGGGTCAATTGTTCTCCTCGCCATCAGGGATCTCAGAG  
GCTCAGAGACTGCAAGCTGCTGCCAAGTCACACAGCTAGTGAAGACAGAGCAGTT  
CTGGTTGTGACTCTAAGCTCAGTGTCTCTCCACTACCCACACCAGCCTTGGTGCCACCAA  
AAGTGTCCCCAAAAGGAAGGAGAATGGATTCTTGAGGCATGCACATCTGGAATTAA  
GTCAAACATTCTCACATCCCTCTAAAGTAAACTACTGTTAGGAACAGCAGTGTCTCAC  
AGTGTGGGGCAGCCGTCTTCTAATGAAGACAATGATATTGACACTGTCCTCTTGGCAGT  
TGCATTAGTAACCTTGAAAGGTATATGACTGAGCGTAGCATA  
CAGGTTAACCTGCAGAAACA  
GTACTTAGGTAATTGTAGGGCGAGGATTATAATGAAATTGCAAACACTTAGCAGCAAC  
TGAAGACAATTATCAACCACGTGGAGAAAATCAAACCGAGCAGGGCTGTGTGAAACATGGTT  
GTAATATGCGACTGCGAACACTGA  
ACTCTACGCCACTCCACAAATGATGTTTCAGGTGTCA  
TGGACTGTTGCCACCATGTATT  
CATCCAGAGTTCTTAAAGTTAAAGTTGACATGATTGTA  
TAAGCATGCTTCTTGAGTTAAATTATGATAA  
ACATAAGTTGCATTAGAAATCAAGC  
ATAAAATCACTCAACTGCAAAAAAAAAAAAAAA

## FIGURE 84

MQRLGATLLCLLLAAAVPTAPAPAPTATSAPVKPGPALSYPQEATLNEMFREVEELMEDTQ  
HKLRSAVEEMEAEEAAKASSEVNLANLPPSYHNETNTDTKGNNTIHVHREIHKITNNQTG  
QMVFSETVITSVGDEEGRSHECIIDEDCGPSMYCQFASFQYTCQPCRGQRMLCTRSECCG  
DQLCVWGHCTKMATRGSNGTICDNQRDCQPGLCCAFQRGLFPVCTPLPVEGELCHDPASRL  
LDLITWELEPDGALDRCPASCGLLCQPHSHSLVYVCKPTFVGSRDQDGIELLPREVPDEYEV  
GSFMEEVQRQLEDLERSLTEEMALGEPAAAAALLGGEI

**Signal sequence:**

amino acids 1-19

**N-glycosylation site.**

amino acids 96-100, 106-110, 121-125, 204-208

**Casein kinase II phosphorylation site.**

amino acids 46-50, 67-71, 98-102, 135-139, 206-210, 312-316,  
327-331

**N-myristoylation site.**

amino acids 202-208, 217-223

**Amidation site.**

amino acids 140-144

## **FIGURE 85**

## **FIGURE 86**

MRLLVAPLLLAWVAGATATVPVVPWHVPCPPQCACQIRPWYTPRSSYREATTVDCCNDLFLTA  
VPPALPAGTQTLLLQSNSIVRVDQSELGYLANLTELDSQNSFSDARDCDFHALPQLLSLHL  
EENQLTRLEDHSFAGLASLQELYLNHNQLYRIAPRAFSGLSNLLRLHLSNLLRAIDSRWFE  
MLPNLEILMIGGNKVDAILDMNFRPLANLRSILVLAGMNLREISDYALEGLQSLSESFYDNQ  
LARVPRRALEQVPGLKFLDLNKNPLQRVGPQDFANMLHLKELGLNNMEELVSI  
DKFALVNLP  
ELTKLDITNNPRLSFIHPRAFHHLQPQMETLMLNNNALSALHQQTVESLPNLQEVGLHGNPIR  
CDCVIRWANATGTRVRFIEPQSTLCAEPPDLQRLPVREVPFREMTDHCLPLISPRSFPPSLQ  
VASGESMVLHCRALAEPEPEIYWVTPAGLRLTPAHAGRRYRVYPEGTLELRRVTAAEAGLYT  
CVAQNLVGA  
DTKTVVVGRALLQPG  
RDEGQGLELRVQETHPYHILLSWVT  
PPNTVSTNL  
TW  
SSASSLRGQGATALARLPRGTHSYNITRLLQATEYWACLQVAFADAHTQLACVWARTKEATS  
CHRALGDRPGLIA  
ILALAVLLAAGLAAHLGTGQPRKG  
VGRRPLPPAWAFWGWSAPS  
VRVV  
SAPLVLPWNPGRKLP  
RSSEGETLLP  
LSQNS

**Signal sequence:**

amino acids 1-18

**Transmembrane domain:**

amino acids 629-648

**N-glycosylation site.**

amino acids 94-98, 381-385, 555-559, 583-587

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 485-489

**Casein kinase II phosphorylation site.**

amino acids 46-50, 51-55, 96-100, 104-108, 130-134, 142-146,  
243-247, 313-317, 488-492, 700-704

**Tyrosine kinase phosphorylation site.**

amino acids 532-540

**N-myristoylation site.**

amino acids 15-21, 493-499, 566-572

**Amidation site.**

amino acids 470-474, 660-664, 692-696

## **FIGURE 87**

GCAAGGCCAAGGCCTGTTGAGAAGGTGAAGAAGTCCGGACCCATGTGGAGGAGGGGACATTGTGTACCGCCT  
CTACATGCCAGACCATCATCAAGGTGATCAAGTTCATCCTCATCTGCTACACCGTCTACTACGTGCACAA  
CATCAAGTTGAGCTGGACTGCACCGTGGACATTGAGAGCCTGACGGGCTACCGCACCTACCGCTGTGCCAACCC  
CCTGGCCACACTCTTCAAGATCCTGGCGTCTTCTACATCAGCCTAGTCATCTTCTACGGCCTCATCGCATGTA  
CACACTGTGGTGGATGCTACGGCGTCCCTCAAGAAGTACTCGTTGAGTCGATCCGTGAGGAGAGCAGCTACAG  
CGACATCCCCGACGTCAAGAACGACTTCGCCTCATGCTGCACCTCATTGACCAATACGACCCGCTACTCCAA  
GCGCTTCGCCGTCTCCTGTCGGAGGTGAGTGAAGAACAGCTGCCAGCTGAACCTCAACAACGAGTGGACGCT  
GGACAAGCTCCGGCAGCGGCTACCAAGAACGCGCAGGACAAGCTGGAGCTGCACCTGTCATGCTCAGTGGCAT  
CCCTGACACTGTGTTGACCTGGTGGAGCTGGAGGTCTCAAGCTGGAGCTGATCCCCGACGTGACCATCCCGCC  
CAGCATTGCCAGCTCACGGCCTCAAGGAGCTGAGGCTTACCCACAGCGGCCAAGATTGAAGCGCTGCGCT  
GCCCTTCTGCGCGAGAACCTGCGGGCGCTGCACATCAAGTTCACCGACATCAAGGAGATCCGCTGTTGATCTA  
TAGCCTGAAGACACTGGAGGAGCTGCACCTGACGGCAACCTGAGCGGGAGAACAAACGCTACATCGTCATCGA  
CGGGCTGCCAGCTCAACGCCCTCAAGGTGTCGGGCTCAAGAGCAACCTAAGCAAGCTGCCACAGTGGTCA  
AGATGTGGGCGTGCACCTGCAAGAGCTGTCATCAACAAATGAGGGACCAAGCTCATGTCCTCAACAGCCTCA  
GAAGATGGCGAACCTGACTGAGCTGGAGCTGATCCGCTGCCACCTGGAGCGCATCCCCACTCCATCTCAGCCT  
CCACAACCTGCGAGGAGATTGACCTCAAGGACAACAAACCTCAAGACCATCGAGGGAGATCATCAGCTTCAGCACCT  
GCACCCGCTCACCTGCCCTAACGCTGTCACACCATGCCCTACATCCCCATCCAGATCGGCAACCTCACCA  
CCTGGAGGCCCTCACCTGAAACCGCAACAAAGATCGAGAAGATCCCCACCCAGCTTCTACTGCCGCAAGCTGCG  
CTACCTGGACCTCAGCCACAAACCTGACCTTCTCCCTGCCACATGCCCTCTGCCAGAACCTCCAGAACCT  
AGCCATCAGGCCAACCGGATCGAGACGCTCCCTCCGGAGCTTCCAGTGGCGGAAGCTGCCGGCTCAGCCT  
GGGCAACAAACGTGTCAGTCAGTCACTGCCCTCCAGGGTGGCGAGCTGACCAACCTGACGAGATCGAGCTGCCGG  
CAACCGCTGGAGTGCCTGCTGTGGAGCTGGCGAGTGCCACTGCTCAAGCGCAGGGCTTGGTGGAGGAG  
GGACCTGTTCAACACACTGCCACCCGAGGTGAAGGAGCGGCTGTGGAGGGCTGACAAGGAGCAGGCTGAGCAG  
GCCGGCCAGCACAGCAAGCAGCAGGACCGCTGCCAGTCTCAGGCCCGAGGGCAGGCTAGCTTCTCCAG  
AACTCCGGACAGCCAGGACAGCCTCGCGGCTGGCAGGGCCTGGGCGCTTGTGAGTCAGGCCAGAGCAGA  
GGACAGTATCTGTGGGCTGGCCCTTTCTCCCTGAGACTCACGCCCAAGGGCAAGTGTGTTGGAGGAG  
AGCAAGTCTCAAGAGCGCAGTATTGGATAATCAGGTCTCTCCCTGGAGGCCAGCTCTGCCCAAGGGCTGAG  
CTGCCACCAGAGGTCTGGGACCTCACTTAGTTCTGGTATTATTATTTCTCCATCTCCACCTCCTCATCC  
AGATAACTTATACATTCCAAGAAAGTTCAGCCAGATGGAAGGTGTCAGGGAAAGGTGGCTGCCCTTCCCC  
TTGTCCATTAGCGATGCCCGGGCATTAAACACCCACCTGGACTTCAGCAGAGTGGCCGGGGCAACCAG  
CCATGGGACGGTCACCCAGCAGTGCCTGGCTCTGAGTTGGCAGTTAGTTTTTTTTTTTTTTTAATCAA  
AAACAATTTTTAAAAAAAGCTTGAATGGATGGTTGGGTATTAAAAAGAAAAAAACTAAAAAAA  
AAAAGACACTAACGCCAGTGTGAGTTGGAGTCTCAGGGCAGGGTGGCAGTTCCCTGAGCAAAGCAGCCAGACGT  
TGAACCTGTTCTTCCCTGGCGCAGGGTGCAGGGTGTCTTCCGGATCTGGTGTGACCTTGGTCCAGGAGTT  
CTATTGTTCTGGGAGGGAGGGAGTTTTGGTTGGTTGGTTGGGTCTTGTGTTCTTCTCCTCC  
ATGTGTCCTGGCAGGCCACTCATTTCTGGCTGCCAGAGGGAAATGTTCTGGAGCTGCCAAGGAGGGAGGAG  
ACTCGGGTTGGCTAATCCCCGATGAAAGGTGCTCATTGCCACCTCCCTCTGTGCCCTGCCCTCTCCA  
CGCACAGTGTAAAGGAGCCAAGAGGAGCCACTTCGCCAGACTTGTGTTCCCTGGCAGGGTGGCTGCTGCC  
CCAGTGCCACCGCTGGCTCCGCTGCTTCCATCAGCCCTGTGCCACCTGGCTTCCATGAAGAGCAGACACTTA  
GAGGCTGGCGGAAATGGGGAGGTGCGCCCTGGGAGGGCAGGGTGGCTGAGTCAAGGCCGGTCCCGTCC  
CTGGAGTGCACACAGCCAGTGGCAGCTGGCTGGAGCCAAGCCACCTGCTTGTGTTAGATCACTCGGGTCCCC  
AGAAGGGTCCCCGCCCTAGATCAATCAGTGGACACTAAGGCACGTTAGAGTCTCTTGTCTTAATGATTATGT  
CCATCCGTCTGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG  
CCTCTGACAACCATGAAGAAAAATCCGTTACATGTGGGCTGAACTGTAGACTCGGTACAGTATCAA  
ATCTATAACAGAAAAAAA

## FIGURE 88

MRQTIIKVIKFILIIICYTVYYVHNIKFDVDCTVDIESLTGYRTYRCAHPLATLFKILASFYI  
SLVIFYGLICMYTLWWMLRRSLKKYSFESIREESSYSDIPDVKNDFAFMLHLIDQYDPLYSK  
RFAVFLSEVSENKLRLQLNNEWTLDKLRQRITKNAQDKLELHLFMLSGIPDTVFVFLVELEV  
LKLELIPDVTIPPSIAQLTGLKELWLYHTAAKIEAPALAFRLRENRLRALHIKFDTIKEIPLWI  
YSLKTLEELHLTGNLSAENNRYIVIDGLRELKRLKVLRLKSNLSKLPQVVTDVGVHLQKLSI  
NNEGTKLIVLNSLKKMANLTELELIRCDLERIPHSIFSLHNLQEIDLKDNNLKTIEEIISFQ  
HLHRLTCLKLWYNHIAYIPIQIGNLTNERLYLNRNKIEKIPQLFYCRKLRYLDLSHNNLT  
FLPADIGLLQNLQNLAITANRIETLPPPELFQCRKLRALHGNVLQSLPSRVGELTNLTQIE  
LRGNRLECLPVELGECPLLKRSGLVVEEDLFNTLPPEVKERLWRADKEQA

**Transmembrane domain:**

amino acids 51-75 (type II)

**N-glycosylation site.**

amino acids 262-266, 290-294, 328-332, 396-400, 432-436, 491-495

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 85-89

**Casein kinase II phosphorylation site.**

amino acids 91-95, 97-101, 177-181, 253-257, 330-334, 364-368,  
398-402, 493-497

**N-myristylation site.**

amino acids 173-179, 261-267, 395-401, 441-447

## **FIGURE 89**

GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCCGT  
CCCGCGGTGGTTGCTGCTGCCGCTGCTGGCCTGAACGCAGGAGCTGTCAATTGACT  
GGCCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCACATG  
TTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCTGGTCAT  
GTGGCTTCAGGGCGGTCCAGGCAGGTTCTAGCACTGGATTGGAAACTTGAGGAAATTGGGC  
CCCTTGACAGTGATCTCAAACCACGGAAAACCACCTGGCTCCAGGCTGCCAGTCTCCTATTT  
GTGGATAATCCCGTGGGCACTGGGTTCAAGTTATGTGAATGGTAGTGGTGCCTATGCCAAGGA  
CCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTCTTCAGTTGCCACAAAG  
AATTCCAGACAGTTCCATTCTACATTTCAGAGTCCTATGGAGGAAAATGGCAGCTGGC  
ATTGGTCTAGAGCTTATAAGGCCATTCAAGCGAGGGACCACAGTGCAACTTGGGGGGT  
TGCCTGGGTGATTCCCTGGATCTCCCTGTTGATTGGTCTCCTGGGGACCTTACCTGT  
ACAGCATGTCCTTCAGAACAAAGGTCTGGCAGAGGTGTCTAAGGGTGCAGAGCAAGTA  
CTGAATGCCGTAAATAAGGGCTCTACAGAGAGGCCACAGAGCTGTGGGGAAAGCAGAAAT  
GATCATTGAACAGAACACAGATGGGTGAACCTCTATAAACATCTTAACTAAAGCACTCCCA  
CGTCTACAATGGAGTCGAGTCAGAATTCAACACAGAGGCCACCTAGTTGTCTTGTCAAGC  
CACGTGAGACACCTACAACGAGATGCCCTAAGCCAGCTCATGAATGGCCCCATCAGAAAGAA  
GCTAAAATTATTCTGAGGATCAATTCTGGGAGGCCAGGCTACCAACGTCTTGTGAACA  
TGGAGGAGGACTTCATGAAGCCAGTCATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATC  
AACGTGACGGTGTATAATGGACAGCTGGATCTCATCGTAGATACCATGGGTCAAGGAGGC  
GGTGGGAAACTGAAGTGGCCAGAACTGCCCTAAATTCAAGTCAGCTGAAGTGGAAAGGCC  
ACAGTGACCCCTAAATCTTGGAAACATCTGCTTTGTCAAGTCCTACAAGAACCTTGCTT  
TACTGGATTCTGAAAGCTGGTCATATGGTCCCTCTGACCAAGGGACATGGCTCTGAAGAT  
GATGAGACTGGTGAECTCAGCAAGAATAGGATGGATGGGCTGGAGATGAGCTGGTTGGC  
TGGGGCACAGAGCTGAGCTGAGGCCCTGAAGCTGTAGGAAGGCCATTCTCCCTGTATCT  
AACTGGGGCTGTGATCAAGAAGGTTCTGACCAAGCTCTGCAGAGGATAAAATCATTGTCT  
GGAGGCAATTGGAAATTATTCTGCTTCTAAAAAAACCTAAGATTTTAAAAAAATTGAT  
TTGTTTGATCAAAATAAGGATGATAATAGATATTAA

## **FIGURE 90**

MELALRRSPVPRWLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATNSC  
KNFSELPLVMWLQGGPGGSSTGFGNFEIGPLSDLKPRKTTWLQAASLLFVDNPVGTGFSY  
VNGSGAYAKDLAMVASDMMVLLKTFFSCHKEFQTVPFYIFSESYGGKMAAGIGLELYKAIQR  
GTIKCNFAGVALGDSWISPDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNAVNGLYRE  
ATELGKAEMIIEQNTDGVNFYNILTKSTPTSTMESSLEFTQSHLVCLCQRHVRHLQRDALS  
QLMNGPIRKKLKIIIPEDQSWGGQATNVFVNMEEDFMKPVISIVDELLEAGINVTVYNGQLDL  
IVDTMGQEAWVRKLKWPELPKFSQLWKALYSDPKSLETSAFVKSYKNLAFYWILKAGHMVP  
SDQGDMALKMMRLVTQQE

**Signal sequence:**

amino acids 1-25

**N-glycosylation site.**

amino acids 64-68, 126-130, 362-366

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 101-105

**Casein kinase II phosphorylation site.**

amino acids 204-208, 220-224, 280-284, 284-288, 351-355, 449-453

**N-myristoylation site.**

amino acids 22-28, 76-82, 79-85, 80-86, 119-125, 169-175,  
187-193, 195-201, 331-337, 332-338, 360-366

## **FIGURE 91**

GGCCGGGGAGAGGAGGCCATGGCGCGCGGGCGCTGCTGCTGGCGCTGCTGGCTC  
GGGCTGGACTCAGGAAGCCGGAGTCGCAGGAGGCGGCCGTTATCAGGACCATGCGGCCGA  
CGGGTCATCACGTGCGCAGTCGTGGTGGAGAGGACGCCGAACTCGGGCGTTGGCCGTGGCA  
GGGGAGCCTGCGCCTGTGGGATTCCCACGTATGCGGAGTGAGCCTGCTCAGCCACCGCTGGG  
CACTCACGGCGGCGCACTGCTTGAAACCTATAGTGACCTTAGTGATCCCTCCGGGTGGATG  
GTCCAGTTGCCAGCTGACTTCCATGCCATCCTCTGGAGCCTGCAGGCCTACTACACCCG  
TTACTTCGTATCGAATATCTATCTGAGCCCTCGTACCTGGGAATTCACCTATGACATTG  
CCTTGGTGAAGCTGTCTGCACCTGTCACCTACACTAAACACATCCAGCCATCTGTCTCCAG  
GCCTCCACATTGAGTTGAGAACCGGACAGACTGCTGGGTGACTGGCTGGGGTACATCAA  
AGAGGATGAGGCAGTGCATCTCCCCACACCCCTCCAGGAAGTTCAGGTGCCATCATAAAC  
ACTCTATGTGCAACCACCTCTCCTCAAGTACAGTTCGCAAGGACATCTTGAGACATG  
GTTTGTGCTGGCAACGCCAAGGCGGGAGGATGCCTGCTCGGTGACTCAGGTGGACCCTT  
GGCCTGTAACAAGAATGGACTGTGGTATCAGATTGGAGTCGTGAGCTGGGAGTGGCTGTG  
GTCGGCCAATCGGCCGGTGTCTACACCAATATCAGCCACCACCTTGAGTGGATCCAGAAG  
CTGATGGCCAGAGTGGCATGTCCCAGCCAGACCCCTCCTGGCCACTACTCTTTCCCTCT  
TCTCTGGCTCTCCACTCCTGGGCCGGTCTGAGCCTACCTGAGCCATGCAGCCTGGGC  
CACTGCCAAGTCAGGCCCTGGTTCTTCTGTCTTGGTAATAAACACATTCCAGTTGA  
TGCCTTGCAGGGCATTCTTCAAAAAAAAAAAAAAAA

## **FIGURE 92**

MGARGALLALLLARAGLRKPESQEAAPLSGPCGRRVITSRIVGGEDAELGRWPWQGSLRLW  
DSHVCGVSLLSHRWALTAAHCFETYSDLSDPSGWMQFGQLTSMPSFWSLQAYYTRYFVSNI  
YLSPRYLGNSPYDIALVKLSAPVTYTKHIQPICLQASTFEFENRTDCWVTGWGYIKEDEALP  
SPHTLQEVAIIINNSMCNHLFLKYSFRKDIFGDMVCAGNAQGGKDACFGDSGGPLACNKNG  
LWYQIGVVSWGVGCGRPNRPGVYTNISHHFEWIQKLMAQSGMSQPDPSWPLLFFPLLWALPL  
LGPV

**Signal sequence:**

amino acids 1-18

**N-glycosylation site.**

amino acids 167-171, 200-204, 273-277

**Casein kinase II phosphorylation site.**

amino acids 86-90, 134-138, 161-165, 190-194, 291-295

**N-myristoylation site.**

amino acids 2-8, 44-50, 101-107, 225-231, 229-235, 239-245,  
259-265, 269-275

**Amidation site.**

amino acids 33-37

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 252-263,

**Serine proteases, trypsin family, histidine active site.**

amino acids 78-84

## **FIGURE 93**

CCACCGCGTCCGGACCGTGGGAAGGGCAGAATGGGACTCCAAGCCTGCCTCTAGGGCT  
CTTGCCCTCATCCTCTGGCAAATGCAGTTACAGCCGGAGCCGACCAGGGAGGACGC  
TGCCCCCAGGCTGGGTGCCCCGGACCTGGAGCTGGCTGAGGAAGAGCTGAGTCTCACCTT  
GCCCTGAGACAGCAGAATGTGGAAAGACTCTGGAGCTGGCTGAGGCTGTGAGGATCCCAG  
CTCTCCTCAATAACGGAAAATACCTGACCCCTAGAGAATGTGGCTTGTGGAGGCCATCCC  
CACTGACCCCTCCACACGGTGCAAAATGGCTCTGGCAGCCGGAGGCCAGAAGTGCCTT  
GTGATCACACAGGACTTCTGACTTGCTGGCTGAGCATCCGACAAGCAGAGCTGCTGCTCCC  
TGGGGCTGAGTTCATCACTATGTGGGAGGACCTACGGAAACCATGTTGTAAGGTCCCCAC  
ATCCCTACCAGCTTCCACAGGCCTGGCCCCCATGTGGACTTGTGGGGGACTGCACCGT  
TTTCCCCAACATCATCCCTGAGGCAACGTCCTGAGCCGAGGTGACAGGGACTGTAGGCCT  
GCATCTGGGTAACCCCTGTGATCCGTAAGCGATACAACCTGACCTACAAGACGTGG  
GCTCTGGCACCAGCAATAACAGCCAAGCCTGTGCCAGTTCCCTGGAGCAGTATTTCCATGAC  
TCAGACCTGGCTCAGTTCATGCGCCTTCGGCAACTTGACATCAGGCATCAGTAGC  
CCGTGTGGTGGACAACAGGGCCGGGGCCGGGATTGAGGCCAGTCTAGATGTGAGT  
ACCTGATGAGTGCTGGTGCACATCTCACCTGGCTACAGTAGCCCTGGCCGGCATGAG  
GGACAGGAGCCCTTCCTGCAGTGGCTCATGCTGCTCAGTAATGAGTCAGCCCTGCCACATGT  
GCATACTGTGAGCTATGGAGATGATGAGGACTCCCTCAGCAGGCCACATCCAGGGTCA  
ACACTGAGCTCATGAAGGCTGCCCTGGGTCTCACCTGCTTCCCTGCCTCAGGTGACAGT  
GGGGCCGGGTGTTGGTCTGTCTGGAAAGACACCAAGCTCCGCCACCTTCCCTGCCTCCAG  
CCCCTATGTCACCACAGTGGAGGCACATCCTCCAGGAACCTTCCTCATCACAAATGAAA  
TTGTTGACTATATCAGTGGTGGCTTCAGCAATGTGTTCCACGGCCTTCATACCAGGAG  
GAAGCTGTAACGAAGTTCTGAGCTAGCCCCCACCTGCCACCATCCAGTTACTTCATGC  
CAGTGGCCGTGCCTACCCAGATGTGGCTGCACCTTGATGGCTACTGGGTGGTCAGCAACA  
GAGTGCCATTCCATGGGTGTCGGAACCTCGCCTCTACTCCAGTGGTTGGGGATCCTA  
TCCTTGATCAATGAGCACAGGATCCTAGTGGCCGCCCCCTTGGCTTCTCAACCCAAG  
GCTCTACCAGCAGCATGGGCAGGTCTTTGATGTAACCGTGGCTGCCATGAGTCCTGTC  
TGGATGAAGAGGTAGAGGGCCAGGGTTCTGCTCTGGCTGGATCCTGTAACAGGC  
TGGGGAACACCAACTCCCAGTTGCTGAAGACTCTACTCAACCCCTGACCCTTCCTATC  
AGGAGAGATGGCTTGTCCCCCTGCCCTGAAGCTGGCAGTTCACTCCCTTATTCTGCCCTGTG  
GAAGCCCTGCTGAACCCCTCAACTATTGACTGCTGCAGACAGCTTATCTCCCTAACCCCTGAAA  
TGCTGTGAGCTTGACTTCAACCCCTACCATGCTCCATCATACTCAGGTCTCCCTACT  
CCTGCCCTAGATTCTCAATAAGATGCTGTAACTAGCATTGGATGCCCTCCCTCCGC  
ATCTCATCTTCTCTTCAATCAGGTTTCAAAGGGTTGTATACAGACTCTGTGACTA  
TTTCACTTGATATTCAATTCCCCAATTCACTGCAAGGAGACCTCTACTGTCACCGTTACTCT  
TTCCTACCCCTGACATCCAGAAACAATGGCCTCCAGTGCATACTTCTCAATCTTGTGTTATG  
GCCTTCCATCATAGTTGCCACTCCCTCTCCTTACTTAGCTTCCAGGTCTTAACCTCTG  
ACTACTCTTGTCTTCTCTCATCAATTCTGCTTCTCATGGAATGCTGACCTCATTG  
TCCATTGAGATTGGCTTCTCAGTTACTCATTGCCCCGGAACAAATCACTGACA  
TCTACAACCATTACCATCTCACTAAATAAGACTTCTATCCAATAATGATTGATAACCTCAA  
TGTAAAAAA

## **FIGURE 94**

MGLQACLLGLFALILSGKCSYSPEPDQRRTLPPGWVSLGRADPEEELSITFALRQQNVERLS  
ELVQAVSDPSSPQYGYLTLENVADLVRPSPLTLHTVQKWLLAAGAQKCHSVITQDFLTCWL  
SIRQAELLLPGAEFHYYVGGPTETHVVRSPHPYQLPQALAPHVDFVGGLHRFPPTSSLRQRP  
EPQVTGTVGHLGVTPSVIRKRYNLTSDVGSCTSNNSQACAQFLEQYFHDSDLAQFMRLFG  
GNFAHQASVARVVGQQGRGRAGIEASLDVQYLMMSAGANISTWVYSSPGRHEGQEPFLQWML  
LSNESALPHVHTVSYGDDEDSLSSAYIQRVNTELMKAAARGLTLFASGDSGAGCWSVSGRH  
QFRPTFPASSPYVTTVGGTSFQEPFLITNEIVDYISGGGFSNVFPRPSYQEEAVTKFLSSSP  
HLPPSSYFNASGRAYPDVAALSDGYWVVSNRVPIPWVSGTSASTPVFGGILSLINEHRILSG  
RPPLGFLNPRLYQQHGAGLFDVTRGCHESCLDEEVEGQGFCSGPGWDPVTGWGTPTSQLC

**Signal sequence:**

amino acids 1-16

**N-glycosylation site.**

amino acids 210-214, 222-226, 286-290, 313-317, 443-447

**Glycosaminoglycan attachment site.**

amino acids 361-365, 408-412, 538-542

**Casein kinase II phosphorylation site.**

amino acids 212-216, 324-328, 392-396, 420-424, 525-529

**N-myristoylation site.**

amino acids 2-8, 107-113, 195-201, 199-205, 217-223, 219-225,  
248-254, 270-276, 284-290, 409-415, 410-416, 473-479, 482-488,  
521-527, 533-539, 549-555

## **FIGURE 95**

GCCGCGCGCTCTCTCCGGCGCCACACCTGTCTGAGCGGCGAGCGAGCCGGCCGGC  
GGGCTGCTCGCGCGGAACAGTGCTCGGCATGGCAGGGATTCCAGGGCTCCTCTCCTTCTC  
TTCTTCTGCTCTGTGCTGTGGCAAGTGAGCCCTACAGTGCCCCCTGGAAACCCACTTG  
GCCTGCATACCGCCTCCCTGTCGTCTGCCCCAGTCTACCCCTCAATTAGCCAAGCCAGACT  
TTGGAGCCGAAGCAAATTAGAAGTATCTTCTCATGTGGACCCCAGTGTCTAAGGGAAC  
CCACTGCCACTTACGAAGAGGCCAAGCAATATCTGTCTTATGAAACGCTCTGCAATGG  
CAGCCGCACAGAGACGCAGGTGGCATCTACATCCTCAGCAGTAGTGGAGATGGGCCAAC  
ACCGAGACTCAGGGTCTTCAGGAAAGTCTCGAAGGAAGCGGCAGATTATGGCTATGACAGC  
AGGTTCAGCATTGGAGGGACTTCCTGCTCAACTACCCCTTCTCAACATCAGTGAAGTT  
ATCCACGGGCTGCACCGCACCCCTGGTGGCAGAGAACGATGTCTCACAGCTGCCACTGCA  
TACACGATGGAAAAACCTATGTGAAAGGAACCCAGAACGCTTCAGCTGGCTTCTAAAGCCC  
AAGTTAAAGATGGTGGTCGAGGGCCAACGACCTCAGCCATGCCAGAGCAGATGAA  
ATTCAGTGGATCCGGTGAAACGCACCCATGTGCCAAGGGTGGATCAAGGGCAATGCCA  
ATGACATCGGCATGGATTATGATTATGCCCTCCTGGAACTCAAAAGCCCCACAAGAGAAAA  
TTTATGAAGATTGGGGTGAGCCCTCTGCTAACGAGCTGCCAGGGGAGAACATTCACTTCTC  
TGGTTATGACAATGACCGACCAGGAATTGGTGTATCGCTTCTGTGACGTCAAAGACGAGA  
CCTATGACTTGCTCTACAGCAATGCGATGCCAGCCAGGGCCAGCGGGTCTGGGTCTAT  
GTGAGGATGTGGAAGAGACAGCAGAACGAGTGGGAGCGAAAAATTATTGGCATTTCAGG  
GCACCAAGTGGTGGACATGAATGGTCCCCACAGGATTCAACGTGGCTGTCAAATCACTC  
CTCTCAAATATGCCAGATTGCTATTGGATTAAAGGAAACTACCTGGATTGTAGGGAGGG  
TGACACAGTGTCCCTGGCAGCAATTAAAGGTCTTCATGTTCTTATTTAGGAGAGGC  
AAATTGTTTTGTCTTGGCGTGCACACGTGTGTGTGTGTGTGTGTGTGTAAAGGTGT  
CTTATAATCTTACCTATTCTTACAATTGCAAGATGACTGGCTTACTATTTGAAAATG  
GTTTGTGTATCATATCATATCATTAAAGCAGTTGAAGGCATACTTTGCATAGAAATAA  
AAAAAAACTGATTGGGGCAATGAGGAATATTGACAATTAAAGTTAATCTTCACGTTTG  
CAAACTTGATTTATTCATCTGAACCTGTTCAAAGATTATTAATATTAAATATTGGCATA  
CAAGAGATATGAAAAA

## FIGURE 96

MAGIPGLLFLLFFLLCAVGQVSPYSAPWKPTWPAYRLPVVLQSTLNLA  
KPDFGAEAKLEVS  
SSCGPQCHKGTPPLPTYEEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRD  
SGSSGKS  
RRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHV  
LTAACIHDGKTYVK  
TQKLRVGFLKP  
KFKDGGRGANDSTS  
AMPEQMKFQWIRVKRTHVPKGWIKGNANDIGMDYD  
YALLELKKPHKRKF  
MKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDV  
KDETYDLLYQQCD  
AQPGASGSGVYVRM  
WKRQQQKWERKIIGIFSGHQW  
VDMNGSPQDFNV  
AVRITPLKYAQIC  
YWIKGNYLDCREG

**Signal sequence:**

amino acids 1-19

**N-glycosylation site.**

amino acids 93-97, 207-211

**Glycosaminoglycan attachment site.**

amino acids 109-113, 316-320

**Casein kinase II phosphorylation site.**

amino acids 77-81, 95-99, 108-112, 280-284, 351-355

**N-myristoylation site.**

amino acids 159-165, 162-168, 202-208, 205-211, 314-320, 338-344

**Serine proteases, trypsin family, histidine active site.**

amino acids 171-177

## FIGURE 97

GCATGCCCTGGGTCTCTCGAGCCTGCTGCCTGCTCCCCGCCACCAGCCATGGTGGTT  
CTGGAGCGCCCCCAGCCCTGGGTGGGGCTGTCTCGCACCTCACCTCCCTGCTGCTGCTG  
GCGTCGACAGCCATCCTCAATGCGGCCAGGATACCTGTTCCCCAGCCTGTGGGAAGCCCCA  
GCAGCTGAACC GGTTGTGGCGGGCGAGGACAGCACTGACAGCGAGTGGCCCTGGATCGTGA  
GCATCCAGAAGAATGGGACCCACCCTGCGCAGGTTCTGCTCACCAAGCCGCTGGGTGATC  
ACTGCTGCCACTGTTCAAGGACAACCTGAACAAACCATACTGTTCTGTGCTGCTGGG  
GGCCTGGCAGCTGGGAACCCCTGGCTCTGGTCCCAGAAGGTGGGTGTTGCCTGGGTGGAGC  
CCCACCCCTGTGTATTCTGGAAAGGAAGGTGCCTGTGCAGACATTGCCCTGGTGCCTCGAG  
CGCTCCATACAGTTCTCAGAGCGGGTCCATGCCCTACCTGATGCCCTATCCACCT  
CCCTCCAAACACCCACTGCTGGATCTCAGGCTGGGGAGCATCCAAGATGGAGTCCCTTGC  
CCCACCCCTCAGACCCTGCAGAACGCTGAAGGTTCTATCATCGACTCGGAAGTCTGCAGCCAT  
CTGTACTGGCGGGAGCAGGACAGGGACCCATCACTGAGGACATGCTGTGCCGGCTACTT  
GGAGGGGGAGCGGGATGCTTGTCTGGCGACTCCGGGGCCCCCTATGTGCCAGGTGGACG  
GCGCCTGGCTGCTGGCCGGCATCATCAGCTGGGGCGAGGGCTGTGCCAGCGAACAGGCC  
GGGGTCTACATCAGCCTCTGCGCACCGCTCTGGGTGGAGAAGATCGTCAAGGGGTGCA  
GCTCCCGGGCGCGCTCAGGGGGTGGGGCCCTCAGGGCACCGAGCCAGGGCTCTGGGGCG  
CCGGCGCTCCTAGGGCGCAGCGGGACCGGGCTCGGATCTGAAAGGCGGCCAGATCCACA  
TCTGGATCTGGATCTGCGCGGCCTCGGGCGGTTCCCCGCCGTAAATAGGCTCATCTACC  
TCTACCTCTGGGGGCCGGACGGCTGCTGCGGAAAGGAAACCCCTCCCCGACCCGCCGAC  
GGCCTCAGGCCCCCTCCAAGGCATCAGGCCCGCCAACGGCCTCATGCCCCGCCAC  
GACTTCCGGCCCCGCCCGGGCCCCAGCGCTTTGTGTATATAATGTTAATGATTATTTAT  
AGGTATTTGTAACCCTGCCCACATATCTTATTATTCCCTCAATTCAATAATTATTATT  
CTCCAAAAAAA

## FIGURE 98

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA43318  
><subunit 1 of 1, 317 aa, 1 stop  
><MW: 33732, pI: 7.90, NX(S/T): 1  
MVVSGAPPALGGGCLGTFTSLLLLASTAILNAARI PVPPACGKPQQLNRVVGGEDSTDSEWP  
WIVSIQKNGTHHCAGSLLTSRWVITAACFKDNLNKPYLF SVLLGAWQLGNPGSRSQKVGVVA  
WVEPHPVYSWKEGACADIALVRLERSIQFSERVLPICLPDASIHLPPNTHCWISGWGSIQDG  
VPLPHPQTLQKLKVPIIDSEVC SHLYWRGAGQGPITEDMLCAGYLEGERDACLGDGGPLMC  
QVDGAWLLAGIISWGEGCAERNRPGVYISLSAHRSWVEKIVQGVQLRGRAQGGGALRAPSQG  
SGAAARS

**Signal sequence:**

amino acids 1-32

**N-glycosylation site.**

amino acids 62-66, 96-100, 214-218, 382-386, 409-413, 455-459,  
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

**Glycosaminoglycan attachment site.**

amino acids 826-830

**Casein kinase II phosphorylation site.**

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,  
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,  
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,  
1013-1017, 1019-1023, 1021-1025

**Tyrosine kinase phosphorylation site.**

amino acids 607-615

**N-myristoylation site.**

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,  
612-618, 623-629, 714-720, 873-879

## **FIGURE 99**

GACGGCTGGCCACCATGCACGGCTCCTGCAGTTCTGATGCTTCTGCTGCCGCTACTGCTA  
CTGCTGGTGGCCACCACAGGGCCCGTTGGAGCCCTCACAGATGAGGAGAACGTTGATGGT  
GGAGCTGCACAACCTCTACCGGGCCAGGTATCCCCGACGGCCTCAGACATGCTGCACATGA  
GATGGGACGAGGAGCTGGCCGCTTCGCCAAGGCCTACGCACGGCAGTGCCTGTGGGCCAC  
AACAAAGGAGCGCGGGCGCCGGCGAGAATCTGTTGCCATCACAGACGAGGGCATGGACGT  
GCCGCTGGCCATGGAGGAGTGGCACCACGAGCGTGAGCACTACAACCTCAGGCCGACCT  
GCAGCCCAGGCCAGATGTGCGGCCACTACACGCAGGTGGTATGGCCAAGACAGAGAGGATC  
GGCTGTGGTCCCACCTCTGTGAGAAAGCTCCAGGGTGTGAGGAGACCAACATCGAATTACT  
GGTGTGCAACTATGAGCCTCCGGGAACGTGAAGGGAAACGCCCTACCAGGAGGGACTC  
CGTGCTCCCAATGTCCCTGGCTACCACTGCAAGAACTCCCTGTGAACCCATCGGAAGC  
CCGGAAGATGCTCAGGATTGCTTACCTGGTAAC TGAGGCCCATCCTCCGGCGACTGA  
AGCATCAGACTCTAGGAAAATGGGTACTCCTCTCCCTAGCAACGGGATTCCGGCTTCT  
TGGTAACAGAGGTCTCAGGCTCCCTGGCAACCAAGGCTCTGCCGTGTGGAAACCCAGGCC  
CCAACTTCTTAGCAACGAAAGACCCGCCCTCCATGGCAACAGAGGCTCACCTGCGTAAC  
AACTGAGGTCCCTCCATTGGCAGCTCACAGCCTGCCCTGGATGAGGAGCCAGTTA  
CCTTCCCCAAATCGACCCATGTTCTATCCAAAATCAGCAGACAAAGTGACAGACAAAACA  
AAAGTGCCCTCTAGGAGCCCAGAGAACTCTCTGGACCCCAAGATGTCCCTGACAGGGCAAG  
GGAACCTCCTACCCCATGCCAGGAGGCTGAGGCTGAGGCTGAGTTGCCCTCCAGTG  
AGGTCTTGGCCTCAGTTTCCAGCCCAGGACAAGCCAGGTGAGCTGCAGGCCACACTGGAC  
CACACGGGCACACCTCCTCCAAGTCCCTGCCAATTCCCCAATACCTCTGCCACCGCTAA  
TGCCACGGGTGGCGTGCCTGGCTTGCAGTCGTCCCTGCCAGGTGCAGAGGCCCTGACA  
AGCCTAGCGTTGTGTCAGGGCTGAACCTGGCCCTGGCATGTGTGGGCCCTCCCTGGGA  
CTACTGCTCCTGCCTCTGGTGTGGCTGGAATCTTCTGAATGGGATACCACCTCAAAGGG  
TGAAGAGGTAGCTGTCCTCTGTCACTTCCCCACCCCTGTCCCCAGGCCCTAAACAAGATA  
CTTCTGGTTAAGGCCCTCCGAAGGGAAAGGCTACGGGCATGTGCCCTCATCACACCCTCC  
ATCCTGGAGGCACAAGGCCTGGCTGGCTGCGAGCTCAGGAGGCCCTGAGGACTGCACACC  
GGGCCACACCTCTCCTGCCCTCCCTGAGTCCTGGGGTGGAGGATTGAGGGAGCT  
CACTGCCTACCTGGCCTGGGCTGTCGCCACACAGCATGTGCGCTCTCCCTGAGTGCCTG  
TGTAGCTGGGGATGGGATTCCCTAGGGCAGATGAAGGACAAGCCCCACTGGAGTGGGTTC  
TTTGAGTGGGGAGGCAGGGACGAGGAAGTAACCTGACTCTCCAATAAAACCT  
GTCCAACCTGTGAAA

## **FIGURE 100**

MHGSCSFLMLLLPLLLLVATTGPVGALTDEEKRLMVELHNLYRAQVSPASDMLHMRWDEE  
LAAFAKAYARQCVWGHNKERGRRGENLFAITDEGMDVPLAMEEWHHEREHYNLSAATCSPGQ  
MCGHYTQVVWAKTERIGCGSHFCEKLQGVEETNIELLVCNYEPPGNVKGKRPYQEGTPCSQC  
PSGYHCKNSLCEPIGSPEADAQDLPYLVTEAPSFRATEASDSRKMGTPSSLATGIPAFLVTEV  
SGSLATKALPAVETQAPTSLATKDPPSMATEAPPCVTTEVPSILAALSPLSLDEEPVTFPKS  
THVPIPKSADKVTDKVPSRSPENSMDPKMSLTGARELLPHAQEEAEAEELPPSSEVLAS  
VFPAQDKPGELQATLDHTGHTSSKSLPNFPNTSATANATGGRALALQSSLPGAECPDKPSVV  
SGLNSGPGHVGPLLGLLLPPLVLAGIF

**Signal sequence:**

amino acids 1-22

**N-glycosylation site.**

amino acids 114-118, 403-407, 409-413

**Glycosaminoglycan attachment site.**

amino acids 439-443

**Casein kinase II phosphorylation site.**

amino acids 29-33, 50-54, 156-160, 195-199, 202-206, 299-303

**N-myristoylation site.**

amino acids 123-129, 143-149, 152-158, 169-175, 180-186, 231-237,  
250-256

**Amidation site.**

amino acids 82-86, 172-176

**Peroxidases proximal heme-ligand signature.**

amino acids 287-298

**Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 1.**

amino acids 127-138

**Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 2.**

amino acids 160-172

## FIGURE 101

GTAACGTGAAAGTCAGGCTTTCATTGGGAAGCCCCCTCAACAGAATTGGTCATTCTCCAAGTTATGGTGGACGT  
ACTTCTGTTCTCCCTCTGTTACATTAGCAGACGGACTTAAGTCACAACAGATTATCTTCAT  
CAAGGCAAGTCCATGAGCCACCTTCAAAGCCTCGAGAAGTGAACACTGAACAATGAATTGGAGACCATCC  
AAATCTGGGACCAAGTCTCGGCAAATATTACACTTCTCTCCTGGCTGGAAACAGGATTGTTGAAATACCTCCCTGA  
ACATCTGAAAGAGTTCACTGAAACTTTGACCTTAGCAGAACAAATATTCAAGAGCTCCAAACTGCATT  
TCCAGCCCTACAGCTCAAATATCTGTATCTCAACAGCAACCGAGTCACATCAATGAAACCTGGTATTTGACAA  
TTTGGCCAACACACTCCTGTGTTAAAGCTGAACAGGAACGAATCTCAGCTATCCCACCCAAAGATGTTAAACT  
GCCCAACTGCAACATCTGAATTGAACCGAAACAAGATTAAAAATGTTAGATGGACTGACATTCCAAGGCCTGG  
TGCTCTGAAAGTCTGAAAGAAATGGACTAACGAAACTATGGATGGAGCTTTGGGGCTGAGCAA  
CATGAAATTTGAGCTGGACCATAACAAACCTAACAGAGATTACCAAGGCTGGCTTACGGCTTGCTGATGCT  
GCAGGAACCTCATCTCAGCCAAATGCCATCAACAGGATCAGCCCTGATGCCCTGGAGTCTGCCAGAAGCTCAG  
TGAGCTGGACCTAACCTTCACTTACAGGTTAGATGATTCAAGCTTCTGGCTTAAGCTTAACTAAC  
ACTGCACATTGGAAACAACAGACTCAGCTACATTGCTGATTGCTCTCCGGGGCTTCCAGTTAAAGACTTT  
GGATCTGAAAGAACATGAAATTCTGGACTATTGAAGACATGAATGGTGTCTCTGGCTTGACAAACTGAG  
GCGACTGATACTCCAAGGAAATCGGATCCGTTCTATTACTAAAAAGCCTTCACTGGTTGGATGCAATTGGAGCA  
TCTAGACCTGAGTGAACACGCAATCATGTCTTACAAGGCAATGCATTTCACAAATGAAGAAACTGCAACAAATT  
GCATTAAATACATCAAGCTTTGTGCGATTGCCAGCTAAATGGCTCCACAGTGGTGGCGAAAACAACCTT  
TCAGAGCTTGTAAATGCAGTTGCCCCATCCTCAGCTGCTAAAGGAAGAAGCATTGCTGTTAGCCCAGA  
TGGCTTGTGTTGATGATTCCAAACCCAGATCACGGTTAGCCAGAACACAGTCGGCAATAAGGTT  
CAATTGAGTTCATCTGCTCAGCTGCCAGCAGTGAATTCCCAATGACTTTGCTTGGAAAAAAAGACAATGA  
ACTACTGCATGATGCTGAAATGGAAAATTATGCAACACCTCCGGGCCAAGGTGGCGAGGTGATGGAGTATACCAC  
CATCCTCGGCTGCGCAGGTGGAATTGCCAGTGAGGGAAATATCAGTGTGTCATCTCCAATCATTGGTTC  
ATCCTACTCTGCAAAGCCAAGCTTACAGTAAATATGCTTCCCTCATTCCAAGACCCCCATGGATCTCACCAT  
CCGAGCTGGGGCATGGCACGCTGGAGTGTGCTGCTGGGGCACCCAGCCCCCAGATAGCCTGGCAGAAGGA  
TGGGGGACAGACTTCCAGCTGCACGGAGAGACGCATGATGATGCCAGGATGACGTGTTCTTATCGT  
GGATGTGAAGATAGAGGACATTGGGTATACAGCTGCACAGCTCAGAACAGTCAGGAAGTATTTCAGCAAATGC  
AACTCTGACTGCTCTAGAAACACCATCATTGCGGCCACTGTTGGACCGAATGTAACCAAGGGAGAAACAGC  
CGTCTACAGTGCATTGCTGGAGGAAGCCCTCCCCCTAAACTGAACCTGGACCAAAGATGATAGCCATTGGTGGT  
AACCGAGAGGCACTTTTGAGCAGGAACTCAGCTTCTGATTATTGTGGACTCAGATGTCAGTGTGCTGGAA  
ATACACATGTGAGATGCTAACACCCCTGGCACTGAGAGAGGAAACGTCAGTGTGATCCCACCTCAAAC  
CTGCGACTCCCCCTCAGATGACGCCACTCGTAGACGATGACGGATGCCACTGTGGGTGTCGTGATCATAGC  
CGTGGTTGCTGTGGGGCACGTCACTCGTGTGGGTGTCATCATACACACAAAGGGGGAGGAATGAAGA  
TTGCAGCATTACCAACACAGATGAGACCAACTTGCAGCAGATATTCTAGTTATTGTGTCATCTCAGGGAACGTT  
AGCTGACAGGCAGGATGGGTACGTGCTTCAGAAAGTGGAAAGCCACCCAGTTGTGTCATCTCAGGTGCTGG  
ATTTTCTTACACACATGACAGTAGTGGACCTGCCATTGACAATAGCAGTGAAGCTGATGTGGAAAGCTGC  
CACAGATCTGTTCTTGTCCGTTTGGGATCCACAGGCCCTATGTATTGAAAGGAAATGTGATGGCTCAGA  
TCCTTGTAAACATATCATACAGGTTGCACTGACCCAGAACAGTTAAATGGACCAACTATGAGCCAGTT  
CATAAAGAAAAAGGAGTGCCTACCATGTTCTCATCCTCAGAAGAACCTGCCAACGGAGCTTCAGTAATATATC  
GTGGCCTTCACATGTGAGGAAGCTACTAACACTAGTTACTCTCACAATGAAGGACCTGGAATGAAAATCTGTG  
TCTAAACAAGTCTCTTGTGAAATGGACCTGCCATTGACAATAGCAGTGAAGCTGATGTGGAAAGCTGC  
TACCTTGGAAAAGCTCTCAGGAGACCTCACCTAGATGCCATTCAAGCTTGGACAGCCATCAGATTGTGAGCC  
AAGAGCCTTTATTGAAAGCTCATCTCCTCCAGACTTGGACTCTGGGTGAGGAAAGATGGAAAGAAAGGAC  
AGATTTCAAGGAAAGAACATCACATTGTACCTTAAACAGACTTTAGAAAACAGACTCCAAATTTCAGTC  
TTATGACTTGGACACATAGACTGAATGAGACCAAAGGAAAAGCTTAACATACACTACCTCAAGTGAACCTTATT  
AAAGAGAGAAATCTTATGTTAAATGGAGTTATGAAATTAAAGGATAAAATGTTATTATACAGAT  
GAACCAAAATTACAAAAAGTTATGAAAATTAAACTGGGAATGATGCTCATATAAGAACACCTTTAAACTA  
TTTTTAACTTGTGTTATGCAAAAAGTATCTACGTAATTAAATGATATAATCATGATTATTTATGTT  
TTATAATGCCAGATTCTTTTATGAAAATGAGTTACTAAAGCATTAAATAACCTGCCATTGACCAATT  
TTAAATAGAAGTTACTTCATTATATTGACATTAAATAATTGTCATTTGAA

## FIGURE 102

MVDVLLFSLCLLFHISRPDLSHNRLSFIKASSMSHLQSLREVKLNNELETIPNLGPVSA  
ITLLSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQTAFPALQLKYLYLNSNRVTSMEP  
GYFDNLANTLLVLKLNRRNRIASIPPKMFKLPQLQHLELNRNKIKNVDGLTFQGLGALKSLKM  
QRNGVTKLMGAFWGLSNMEILQLDHNNLTEITKGWLGYLLMLQELHLSQNAIRISPD  
FCQKLSELDLTFNHLRLDDSSFLGLSLLNTLHIGNNRVSYIADCAFRLSSLKTLDDLKNNE  
ISWTIEDMNGAFSGLDKLRRLILQGNRIRSITKKAFTGDALEHLDLSDNAIMSLQGNAFSQ  
MKKLQQLHLNTSSLLCDCQLKWLQPQWVAENNQSFVNASCAPQLLKGRSIFAVSPDGFVCD  
DFPKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKKDNELLHDAEMENYAHLRAQG  
GEVMEYTTILRLREVEFASEGKYQCVISNHFGSSYSVAKLTVNMLPSFTKTPMDLTIRAGA  
MARLECAAVGHPAPQIAWQKDGGTDFPAAERRMHVMPEDDVFFIVDVKIEDIGVYSCTAQN  
SAGSISANATLTVLETPSFLRPLLDRVTKGETAVLQCIAGGSPPPKNWTKDDSPLVTER  
HFFAAGNQLLIVDSDVSAGKYTCEMSNTLGETGNVRLSVIPTPTCDSPQMTAPSLLDDG  
WATVGVVIIAVVCCVVGTSLVWVVIYHTRRRNEDCSITNTDETNLPADIPSYLSSQGTLAD  
RQDGYVSSESGSHHQFVTSSGAGFFLPQHDSSGTCHIDNSSEADVEAATDLCFLCPFLGSTGP  
MYLKGNVYGSDFETYHTGCPDPRTVLMDHYEPSYIKKKECYPCHPSEESCERSFSNISW  
PSHVRKLLNTSYSHNEGPGMKNLCLNKSSLDFSANPEPASVASSNSFMGTFGKALRRPHLDA  
YSSFGQPSDCQPRAFYLKAHSSPDLDGSEEDGKERTDFQEENHICTFKQTLENYRTPNFQS  
YDLDT

**Signal sequence:**

amino acids 1-19

**Transmembrane domain:**

amino acids 746-765

**N-glycosylation site.**

amino acids 62-66, 96-100, 214-220, 382-386, 409-413, 455-459,  
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

**Glycosaminoglycan attachment site.**

amino acids 826-830

**Casein kinase II phosphorylation site.**

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,  
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,  
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,  
1013-1017, 1019-1023, 1021-1025

**Tyrosine kinase phosphorylation site.**

amino acids 607-615

**N-myristoylation site.**

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,  
612-618, 623-629, 714-720, 873-879

## **FIGURE 103**

GGGGAGAGGAATTGACCATGTAAGGAGACTTTTTGGTGGTGGCTGTTGGGTGCCTTGCAAAATG  
AAGGATGCAGGACGCAGCTTCTCTGGAACCGAACGCAATGGATAAAACTGATTGTGCAAGAGAGAAGGAAGAAC  
GAAGCTTTCTGTGAGCCCTGGATCTAACACAAATGTGTATATGTGCACACAGGGAGCATTCAAGAATGAAA  
TAAACCAGAGTAGACCCCGGGGGTTGGTGTGTTCTGACATAAATAATCTTAAAGCAGCTGTTCCCCCTCC  
CCACCCCCAAAAAAAGGATGATTGGAAATGAAGAACCGAGGATTACAAAGAAAAAGTATGTTCTTTTCTC  
TATAAAGGAGAAAGTGAAGCCAAGGGAGATATTTGGAAATGAAAAGTTGGGGCTTTTAGTAAAGTAAAGAAGT  
GGTGTGGTGGTGTTCCTTCTTTGAATTCCACAAAGAGGGAGGAAATTAAATAATACATCTGCAAAGAAA  
TTTCAGAGAAGGAAAGTGAACCGGGCAGATTGAGGCATTGATTGGGGAGAGGAAACCCAGCAGGACAGTTGGA  
TTTGTGCTATGTTGACTAAATTGACGGATAATTGACGGATTGGGATTTCTTCATCAACCTCCTTTTTAAAT  
TTTATTCTCTTGGTATCAAGATCATGCGTTTCTCTTGTCTTAACCAACCTGGATTTCATCTGGATGTTGCT  
GTGATCAGTCTGAAATACAACACTGTTGAATTCCAGAACGGGAAACACAGATAAAATTATGAATGTTGAACAAGAT  
GACCTTACATCCACAGCAGATAATGATAGGTCTAGGTTAACAGGGCCCTATTGACCCCTGCTTGTGGT  
GCTGGCTCTCAACTCTGTGGTGGCTGGTCTGGTGGGGCTCAGACCTGCCCTCTGTGCTCTGCAGCAA  
CCAGTTCAAGGTGATTGTGTTGGAAAACCTCGGTGAGGTCGGATGGCATCTCCACCAACACAGGCT  
GCTGAACCTCCATGAGAACCAAATCCAGATCATCAAAGTGAACAGCTCAAGCAGTTGAGGGACTTGGAAATCCT  
ACAGTTGAGTAGGAACCATATCAGAACCAATTGGAAATTGGGGCTTCAATGGTCTGGGAACCTCAACACTTGGA  
ACTCTTGACAATCGTCTACTACCATTCCGAATGGAGCTTTGTATACTTGCTAACTGAAGGAGCTTGTT  
GCGAAACAACCCATTGAAAGCATCCCTCTTATGCTTTAACAGAACTCCTCTTGCCTCGACTAGACTTAGG  
GGAATTGAAAAGACTTCATACATCTCAGAACGGTGCCTTGAAGGTCTGTCCAACCTGAGGTATTGAAACCTTGC  
CATGTGCAACCTCGGGAAATCCCTAACCTCACACCGCTCATAAAACATGAGCTGGATCTTCTGGGAATCA  
TTTATCTGCCATCAGGCTGGCTTTCCAGGGTTGATGCACCTCAAAACTGTGGATGATACAGTCCCAGAT  
TCAAGTGATTGAACGGAATGCCCTTGACAACCTTCAGTCACTAGTGGAGATCAACCTGGCACACAATAATCTAAC  
ATTACTGCCATGACCTTCACTCCCTGATCATCTAGAGCGATACATTACATCACACCCCTTGGAAACTG  
TAACGTGACATACTGTGGCTCAGCTGGTGGATAAAAGACATGGCCCCCTGAACACAGCTTGTGCTCCGGT  
TAACACTCCTCCAATCTAAAGGGGAGGTACATTGGAGAGCTGACCAGAAATTACTTCACATGCTATGCTCCGGT  
GATTGTGGAGCCCCCTGCAGACCTCAATGTCAGTCAAGGCATGGCAGCTGAGGTGAAATGTCGGGCCTCCACATC  
CCTGACATCTGTATCTGGATTACTCCAAATGGAACAGTCAGTACATGGCGTACAAAGTGCAGATAGCTGT  
GCTCAGTGTGGTACGTTAAATTTCACAAATGTAACCTGTGCAAGATACAGGCATGTACACATGTATGGTGGTAA  
TTCGGTTGGAAACTACTGCTTCAGCCACCTGAATGTTACTGCAGCAACCAACTCTCTTCTTACTTTTCA  
AACCGTCACAGTAGAGACTATGGAAACCGTCTAGGATGAGGACGGGACACAGATAACAAATGTGGGTCCCACCTC  
AGTGGTCAGTGGAGACCAACTGTGACCACTCTCACACCAACAGAGCACAAAGTCAGAGGAAACCTT  
CACCATCCCAGTGACTGATATAAACAGTGGATCCCAGGAATTGATGAGGTGATGAGACTACCAAAATCATCAT  
TGGGTGTTGTGGCCATCACACTCATGGCTGCACTGATGCTGGTCATTTCATCAAGATGAGGAAGCAGCACCA  
TCGGAAAACCATCACGCCAACAGGACTGTTGAAATTATTAATGTGGATGAGGTTACGGGAGACACACC  
CATGGAAAGCCACCTGCCATGCCCTGCTATCGAGCATGAGCACCTAAATCACTATAACTCATCAAATCTCCCTT  
CAACCACACAACAGTTAACACAATAATTCAATACACAGTTCACTGATGAAACCGTATTGATCCGAATGAA  
CTCTAAAGACAATGTACAAGAGACTCAAATCTAAACATTACAGAGTTACAAAAAAACAAATCAAAAAAA  
GACAGTTATTAAGACACAAATGACTGGCTAAATCTACTGTTCAAAAAAGTGTCTTACAAAAAAACAA  
AAAAGAAAAGAAATTATTTATTGATCTAAAGCAGACAAAAA

## **FIGURE 104**

MLNKMTLHPQQIMIGPRFNRALFDPLLVLLALQLLVAGLVRAQTCPSVCSCSNQFSKVIC  
VRKNLREVPDGISTNTRLLNLHENQIQIICKVNSFKHLRHEILQLSRNHIRTIEIGAFNGLA  
NLNTLELFDNRLTTIPNGAFVYLSKLKELWLRNNPIESIPSYAFNRIPSLRRLDLGELKRLS  
YISEGAFEGLSNLRYLNLCNLREIPNLTPLIKLDELDLSGNHLSAIRPGSFQGLMHLQKL  
WMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPPLHHLERIHLHHNPWNCNDIL  
WLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNVTGMAAE  
LKCRASTSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTQDTGMYTCMVSNSVGN  
TTASATLNVTAATTPFSYFSTVTETMEPSQDEARTTDNNVGPTPVVDWETTNVTTSLTPQ  
STRSTEKTFTIPVTDINSGIPGIDEVMKTTKIIIGCFVAITLMAAVMLVIFYKMRKQHHRQN  
HHAPTRTVEIINVDEITGDTPMESHLPMPAIEHEHLNHNSYKSPFNHTTVNTINSIHSS  
VHEPLLIRMNSKDNVQETQI

**Signal sequence:**

amino acids 1-44

**Transmembrane domain:**

amino acids 523-543

**N-glycosylation site.**

amino acids 278-282, 364-368, 390-394, 412-416, 415-419, 434-438,  
442-446, 488-492, 606-610

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 183-187

**Casein kinase II phosphorylation site.**

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

**N-myristoylation site.**

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,  
391-397, 422-428, 433-439, 531-537

## FIGURE 105

AGCCGACGCTGCTCAAGCTGCAACTCTGTCAGTGGCAGTTCTTCCGTTCCCTGCTGTTGGGGCA  
TGAAAGGGCTTCGCCGCCGGAGTAAAAGAAGGAATTGACCGGGCAGCGCAGGGAGGAGCGCGCACCGCACCG  
GAGGGCGGGCGTGACCCCTCGGCTGGAGTTGTGCCCCGGCCCGAGCGCGCCGGCTGGAGCTGGTAGA  
GACCTAGGCCCTGGACCGCGATGAGCGCGAGCCTCCGTGCGCGCCGGCTGGAGCTGGTAGCGCTGTGC  
GCGGTGCTGGGGCGCTGGCCGGTCCGACAGCGGGCGTGGAGCTGGAGCTGGACTGAGCTGTAAGCGCTAGCGCT  
GAGCGCCCATGCCCACTACCGCCGCGTGCCTCGGGGACCTGCTGGACTTAAGTCACAACAGATTATCTTCAAGGCAAGTCC  
CCCGAGCCACTCCCCTCGCTGGGTGCGCTGGACTTAAGTCACAACAGATTATCTTCAAGGCAAGTCC  
ATGAGCCACCTTCAAAGCTTCGAGAAGTGAACACAATGAATTGGAGACCAATTCAAATCTGGGACCA  
GTCTCGGCAAATATTACACTTCTCTTGGCTGAAACAGGATTGTGAAATACTCCCTGAACATCTGAAAGAG  
TTTCAGTCCCTGAAACATTGGACCTTAGCAGCAACAAATTTAGCAGCTCAAACAGTCAAATCCAGCCCTACAG  
CTCAAATATCTGTATCTAACAGCAACCGAGTCACATCAATGAAACCTGGGTTAGTGTGAAATTTGGGCAACACA  
CTCCTGTGTTAAAGCTGAAACAGGAACCGAATCTCAGCTATCCCACCCAAAGATGTTAAACTGCCCCACTGCAA  
CATCTCGAATTGAAACCGAAACAAGATTAAAATGTAGATGGACTGACATTCCAAGGCTTGGTCTGAAAGTCT  
CTGAAAATGCAAAGAAATGGAGTAACGAAACTTATGGATGGACTTTTGGGGCTGAGCAACATGGAAATTG  
CAGCTGGACCATAACAAACCTAACAGAGATTACCAAAGGCTGGCTTACGGCTGCTGAGTGTGAGCTGGACCT  
CTCAGCCAAATGCCATCAACAGGATCAGCCCTGATGCTGGAGTTCTGCCAGAAGCTCAGTGAAGCTGGACCTA  
ACTTCAATCACTTATCAAGGTTAGATGATTCAAGCTTCTGGCCTAAGCTTACTAAATACACTGACATTGG  
AAACAACAGAGTCAGCTACATTGCTGATTGTGCCCTTCCGGGGCTTCCAGTTAAAGACTTGGATCTGAAAGAAC  
AATGAAATTCTGGACTATTGAAGACATGAATGGTCTTCTGGGCTGACAAACTGAGGCAGCTGATAACTC  
CAAGGAAATCGGATCCGTTCTATTACTAAAAAAGCCTTCACTGGTTGGATGCAATTGGAGCATAGACCTGAGT  
GACAACGCAATCATGTTACAAGGCAATGCAATTTCACAAATGAAGAAACTGCAACAATTGCAATTAAATACA  
TCAAGCCTTTGTGCGATTGCCAGCTAAATGGCTCCACAGTGGTGGCGAAAACAACACTTCAAGGCTTGT  
AATGCCAGTTGTGCCCATCCTCAGCTGCTAAAGGAAGAACGATTGGTCTGTTAGCCAGATGGCTTGTG  
GATGATTTCACCAACCCAGATCACGGTCAGCCAGAAACACAGTCGGCAATAAAAGGTTCCAATTGAGTTTC  
ATCTGCTCAGCTGCCAGCAGCAGTGATTCCCAATGACTTTGCTGGAAAAAGACAATGAACTACTGCA  
GCTGAAATGGAAAATTATGCAACACCTCCGGGGCCAAGGTGGCGAGGTGATGGAGTATACCACCATCCTCGGCTG  
CGCAGGGTGGAAATTGCCAGTGAGGGAAATATCAGTGTGTCATCTCCAATCACATTGGTCTCATC  
AAAGCCAAGCTTACAGTAAATATGCTTCCCTATTCCAAGAACGCCCCATGGATCTC  
ATGGCACGCTGGAGTGCTGCTGCTGGGCAACCCAGCCCCAGATAGCCTGGCAGAAGGATGGGGCACAGAC  
TTCCAGCTGACGGAGAGACGATGCACTGTGATGCCAGGGATGAGTCTTATGTTGAGATA  
GAGGACATTGGGTATACAGCTGACAGCTCAGAACAGTGCAGGAAGTATTCTAGCAAATGCAACTCTGACTGTC  
CTAGAAACACCATCATTTGCGGCCACTGTTGGACCGAATGTAACCAAGGGAGAACAGCGTCTACAGTGC  
ATTGCTGGAGGAAGCCCTCCCCCTAAACTGAACTGGACCAAGAGTATGCCATTGGTGGTAACCGAGAGGCAC  
TTTTTGAGCAGGCAATCAGCTCTGATTATTGAGACTCAGATGTCAGTGTGACTGGAAATACACATGTGAG  
ATGCTAACACCCCTGGCACTGAGAGAGGAAACGTGCCCTCAGTGTGATCCCCACTCCAACCTGCA  
CAGATGACAGCCCCATCGTAGACGATGACGGATGGGCCACTGTGGGTGCTGATCATAGCGTGGTTGCTG  
GTGGGGCACGTCACTCGTGTGGTGTATCATATACCACACAAGCGGAGGAATGAAGATTGAGCATTAC  
AACACAGATGAGACCAACTGCCAGCAGATATTCTAGTTATTGTCATCTCAGGGAACGTTAGCTGACAGGAG  
GATGGGTACGTGCTTCAGAAAGTGGAAAGCCACCAAGTTGTACATCTCAGGTGCTGGATTTC  
CAACATGACAGTAGTGGACCTGCCATTGACAATAGCAGTGAAGCTGATGAGCTGCCACAGATCTGTC  
CTTGCCCTTTGGGATCCACAGGCCATTGATTTGAAGGGAAATGTGATGGCTCAGATCCTTGA  
TATCATACAGGGTGCAGCTCTGACCCAAGAACAGTTTAATGGACCACTATGAGGCCAGTTACATAAAGAAAAG  
GAGTGTACCCATGTTCTCATCTTCAAGAACAGTCAATCTCGGAACGGAGCTCAGTAATATATCGTGGCCT  
GTGAGGAAGCTTAAACACTAGTTACTCTCAGAACAGTGAAGGACCTGGAAATGAAAAATCTGTTGCTAAACAAGTCC  
TCTTAGATTAGTGCACATCCAGAGCCAGCGCTGGTGCCTCGAGTAATTCTTCTAGGGTACCTTTGGAAAAA  
GCTCTCAGGAGACCTCACCTAGATGCCATTCAAGCTTGGACAGCCATCAGATTGTCAGCCAAGAGCCTT  
TTGAAAGCTCATTCTCCCCAGACTGGACTCTGGTCAAGAGGAAGATGGGAAAGAACAGATTTCAGGAA  
GAAAATCACATTGTACCTTAAACAGACTTAAAGAAAACAGTCAACATACCTCAAGTGAACCTT  
ACATAGACTGAATGAGACCAAGGAAAAGCTTAAACATACCTCAAGTGAACCTT  
CTTATGTTAAATGGAGTTATGAATTAAAGGATAAAAATGCTTATTATACAGATGAACCCAAATTAC  
AAAAAGTTATGAAAATTTTATACTGGGAATGATGCTCATATAAGAAATACCTTAAACTATT  
TTTATGCAAAAAGTATCTACGTAATTAAATGATATAATCATGATTATTGTTATGTTATAATGCCAGA  
TTCTTTTATGAAAATGAGTTACTAAAGCATTAAATAACCTGCCCTGTACCATTTAAATAGAAGTT  
ACTCATTATATTGACATTATTAATAAAATGTGCAATTGAAAAA

## **FIGURE 106**

MSAPSLRARAAGLGLLLCAVLGRAGRSDSGGRGELGQPSGVAERPCPTTCRCLGDLDCSR  
KRLARLPEPLPSWVARLDLSHNRLSFIKASSMSHLQLSREVKLNNELETIPNLGPVSANIT  
LLSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQTAFPALQLKYLYLNSNRVTSMEPGY  
FDNLANTLLVLKLNRRNRIASIPPKMFKLPQLQHLELNRNKIKNVGGLTFQGLGALKSLKMQR  
NGVTKLMGAFWGLSNMEILQLDHNNLTEITKGWLYGLLMLQELHLSQNAINRISPDAWEFC  
QKLSELDLTFNHLSRLDDSSFLGLSLLNLTIGHNNRVSYIADCAFRLSSLKTLIDLKNNEIS  
WTIEDMNGAFSGLDKLRRILQGNRIRSITKKAFTGILDALEHLDLSDNAIMSLQGNAFSQMK  
KLQLHLNTSSLCDCQLKWLPOVVAENNQSFVNASCAPQQLKGRSIFAVSPDGFVCDDF  
PKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAKKDNELLHDAEMENYAHLRAQGGE  
VMEYTTILRLREVEFASEGKYQCVISNHFGSSYSVKAKLTVNMLPSFTKTPMDLTIRAGAMA  
RLECAAVGHPAPQIAWQKDGGTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYSCTAQNSA  
GSISANATLTVLETPSFLRPLLDRVTKGETAVLQCIAGGSPPPKNWTKDDSPLVVTERHF  
FAAGNQLLIIVSDVSDAGKYTCMSNTLGTTERGNVRLSVIPTPTCDSPQMTAPSLLDDGWA  
TVGVVIIAVVCCVVGTSLVWVVIYHTRRNEDCSITNTDETNLPADIPSYLSSQGTLADRO  
DGYVSSESGSHHQFVTSAGFFLPQHDSSGTCHIDNSSEADVEAATDLFCLCPFLGSTGPMY  
LKGNVYGSDFETYHTGCSPDPRTVLMHYEPSYIKKKECYPCHPSEESCRSFSNISWPS  
HVRKLLNTSYSHNEGPGMKNLCLNKSSLDFSANPEPASVASSNSFMGTFGKALRRPHLDAYS  
SFGQPSDCQPRAFYLAHSSPDLDGSEEDGKERTDFQEENHICTFKQTLHENYRTPNFQSYDLDT

**Signal sequence:**

amino acids 1-27

**Transmembrane domain:**

amino acids 808-828

**N-glycosylation site.**

amino acids 122-126, 156-160, 274-278, 442-446, 469-473, 515-519, 688-692, 729-733, 905-909, 987-991, 999-1003, 1016-1020

**Glycosaminoglycan attachment site.**

amino acids 886-890

**Casein kinase II phosphorylation site.**

amino acids 99-103, 180-184, 263-267, 314-318, 324-328, 374-378, 383-387, 407-411, 524-528, 608-612, 692-696, 709-713, 731-735, 799-803, 843-847, 863-867, 907-911, 1003-1007, 1018-1022, 1073-1077, 1079-1083, 1081-1085

**Tyrosine kinase phosphorylation site.**

amino acids 667-675

**N-myristoylation site.**

amino acids 14-20, 36-42, 239-245, 257-263, 380-386, 427-433, 513-519, 588-594, 672-678, 683-687, 774-780, 933-939

**Leucine zipper pattern.**

amino acids 58-80, 65-87

## FIGURE 107

CAAAACTTGCCTCGCGAGAGCGCCAGCTGACTTGAATGGAAGGAGCCCAGGCCGAGCCGCGAGCGCAGCTGAGAC  
TGGGGGAGCGCTTCGGCCTGTGGGCGCCGCTGGCAGGGGGCGCAGCAGGGAAAGGGGAAGCTGTGGTCTGCC  
CTGCTCCACGAGGCGCCACTGGTGTGAACCGGGAGAGCCTGGTCCCGTCCCCTATCCCTCTTTATATA  
GAAACCTTCCACACTGGGAAGGCAGCGGAGGGCTATGGTGAGCAAGGAGGCCGCTGATCTGAG  
GCGCACAGCATTGGAGTTACAGATTTACAGATACCAAATGGAAGGCAGGGAGGCAGAACAGCCTGCCCTGGT  
TCCATCAGCCCTGGCGCCAGGCGCATCTGACTCGGCACCCCTGAGGCACCATGGCCAGAGGCCGGTGTGC  
TGCTCCTGCTGCTGCGCCACAGCTGACCTGGGACCTGTGCTTGCGTGAGGGCCCGAGGATTTGGCCGAA  
GTGGCGGCCACAGCCTGAGCCCCGAAGAGAACGAATTGCGGAGGGAGGCCGTGCTGTAAGGCCCTGAGG  
AGCCCGGGCTGGCCAGCCGGTCAGCTGCCCGAGACTGTGCTGTTCCAGGAGGGCGTGTGACTGTG  
GCGGATTGACCTGCGTGAAGTCCCCGGGGACCTGCGCTGAGCACACCAACCCATCTGCAGAACACACCAGC  
TGGAAAGATCTACCCCTGAGGAGCTCTCCGGCTGACCCGGCTGGAGAGACACTGAAACCTGCAAAACAAACCGCCTGA  
CTTCCCAGGGCTCCAGAGAACGGCTTGAGCATCTGACCAACCTCAATTACCTGTAAGTGGCCAATAACAAGC  
TGACCTTGGCACCCGCTTCCCTGCCAAACGCCCTGATCAGTGGACTTGTGCTGCCAAACTATCTCACCAAGATCT  
ATGGGCTCACCTTGGCAGAACGCAAACCTGAGGTCTGTGACTCTGCACAAACAAACAGCTGGCAGACGCCGGC  
TGCCGGACAAACATGTCACGGCTCAGCAACGTCAGGGTCTCATCCTGTCAGCAACTTCCCTGCGCCACGTGC  
CCAAGCACCTGCCCTGTCACAGCTGACCTCAAGAACAAACAGCTGGAGAACAGATCCCCGGGGCCT  
TCAGCGAGCTGAGCAGCTGCGAGCTATACTGCAGAACAAACTACCTGACTGACGAGGCCGCTGGACAAACGAGA  
CCTCTGGAAGCTCTCAGCCTGGAGTACCTGGATCTGTCAGCAACACCTGTCTGGGTCCCAGCTGGCTGC  
CGCGCAGCCTGGTGTGCTGCACTGGAGAACGACGCCATCCGGAGCGTGGACGCGAATGTGCTGACCCCCATCC  
GCAGCCTGGAGTACCTGCTGTCACAGCAACAGCTGCCAGGAGCAGGGCATCCACCCACTGGCCTCCAGGGCC  
TCAAGCGGTTGACACGGTGACCTGTACAACAAACCGCTGGAGGCCGTTGGCCTGCGCTGC  
GCACCCCTCATGATCCTGCACAACCAGATCACAGGCAATTGGCGCGAAGACTTGGCACCACCTACTTGGAGG  
AGCTAACCTCAGCTACAACCGCATCACCAGCCCACAGGTGACCGCCTCCGCAAGCTGCCCTGCTGC  
GCTCGCTGGACCTGTCGGCAACCAGCTGCACACGCTGCCACCTGGCTGCCATGGAAATGTCATGTGCTGAAGG  
TCAAGCGCAATGAGCTGGCTGCCTTGGCACAGGGGGCGCTGGCGGGCATGGCTCAGCTGCGTGAGCTGTACCTCA  
CCAGCAACCGACTGCGCAGCCCTGGGCCCCCTGCTGGTGGACCTGCCCATCTGCAGCTGCTGGACA  
TCGCCGGAAATCAGCTCACAGAGATCCCCGAGGGCTCCCCGAGTCACCTGAGTACCTGTCAGAACACA  
AGATTAGTGGCTGCCGCCAACGCTTCGACTCCACGCCAACCTCAAGGGATCTTCTCAGGTTAACAAAGC  
TGGCTGTGGCTCCGTGGACAGTGCCTTCCGGAGGCTGAAGCACCTGCAAGGTCTTGGACATTGAAGGCAACT  
TAGAGTTGGTGAACATTCCAAAGGACCGTGGCGCTTGGGAAGGAAAGGAGGAGGAGGAAGAGGAGGAGGAGG  
AGGAAGAGGAAACAAAGATAGTGAACAGGTGATGCAGATGTGACCTAGGATGATGGACCGGGACTTTCTGC  
AGCACACGCCCTGTGCTGAGCCCCCACTCTGCCGTGTCACACAGACACACCCAGCTGCACACATGAGGCA  
TCCCACATGACACGGCTGACACAGCTCATATCCCCACCCCTGCCACGGCGTGTCCCACGGCCAGACACATGC  
ACACACATCACACCCCTCAAACACCCAGCTCAGCCACACACAACACTACCCCTCCAAACCCACAGTCTGTACAC  
CCCCACTACCGCTGCCACGCCCTGTAATCATGCAGGGAAAGGGCTGCCCTGCCATGGCACACACAGGCCACCA  
TCCCCTCCCCCTGCTGACATGTGATGCGTATGCATACACACCACACACACATGCAACAGTCATGTGCGAA  
CAGCCCTCCAAAGCTATGCCACAGACAGCTTGTGCCAGGCCAGAACATGCCATAGCAGCTGCCGTGCC  
GTCCCATCTGCCGTCCGTTCCCTGGAGAACACAAGGTATCCATGCTCTGTGGCCAGGTGCCCTGCCACCCCT  
GGAACTCACAAAAGCTGGTTTATTCTTCCATCCTATGGGGACAGGAGGCCCTCAGGACTGCTGGCTGCC  
TGGCCACCCCTGCTCCAGGTGCTGGGAGTCACCTGCTAAGAGTCCCTCCCTGCCACGCCCTGGCAGGACA  
CAGGCACTTTCCAATGGGCAAGCCAGTGGAGGGCAGGATGGGAGAGGCCCTGGGTGCTGCTGGGGCTTGGGG  
CAGGAGTGAAGCAGAGGTGATGGGGCTGGCTGAGCCAGGGAGGAAGGACCCAGCTGCACCTAGGAGAACCTT  
GTTCTCAGGCCTGTGGGGAAAGTCCGGTGCCTTATTCTTATTCTTCTAAGGAAAAAAATGATAAAAAT  
CTCAAAGCTGATTTCTTGTATAGAAAACATAATAAAAGCATTATCCCTATCCCTGCAAAAAAA

## FIGURE 108

MEGEEAEQPAWFHQWPWRPGASDSAPPAGTMAQSRVLLLLLPPQLHLGPVLAVRAPGFGRS  
GGHSLSPPEENEFAEEEPVLVLSPEEPGPGPAAVSCPRDCACSQEGVVDCGGIDLREFPGDLP  
EHTNHLSLQNNQLEKIYPEELSRLHRLETNLQNNRLTSRGLPEKAFEHTNLNYLYLANNK  
LTLaPRFLPNALISVDFAANYLTKIYGLTFGQKPNLRSVYLHNNKLADAGLPDNMFNGSSNV  
EVLILSSNFLRHVPKHLPPALYKLHLKNNKLEKIPPGAFSELSSLRELYLQNNYLTDEGLDN  
ETFWKLSSLEYLDLSSNNLSRVPAGLPRSLVLLHLEKNAIRSVDANVLPIRSLEYLLLHSN  
QLREQGIHPLAFQGLKRLHTVHLYNNALERVPSGLPDRVTLMILHNQITGIGREDFATTYF  
LEELNLSYNRITSQPQVHRDAFRKLRLRSLDLSGNRLHTLPPGLPRNVHVLKVKRNEALAALA  
RGALAGMAQLRELYLTSNRLRSRALGPRAWVDLAHLQLLDIAGNQLTEIPEGLPESLEYLYL  
QNNKISAVPANAFDSTPNLKGIFLRFNKLAVGSVVDSAFRRLKHLQVLDIEGNLEFGDISKD  
RGRLGKEKEEEEEEEEEEETR

**Signal sequence:**

amino acids 1-48

**N-glycosylation site.**

amino acids 243-247, 310-314, 328-332, 439-443

**Casein kinase II phosphorylation site.**

amino acids 68-72, 84-88, 246-250, 292-296, 317-321, 591-595

**N-myristoylation site.**

amino acids 19-25, 107-113, 213-219, 217-223, 236-242, 335-341,  
477-483, 498-502, 539-545, 548-554

**Leucine zipper pattern.**

amino acids 116-138, 251-273, 258-280, 322-344, 464-486, 471-493,  
535-557

## FIGURE 109

GGGAGGGGGCTCCGGGCGCCGCGCAGCAGACTGCTCCGGCGCGCCTGCCGCTGCTCTCCGGGAGCGGCAG  
CAGTAGCCGGGCGAGGGCTGGGGTTCTCGAGACTCTCAGAGGGCGCCTCCCATGGCGCCACCACCC  
CAACCTGTTCTCGCGCCCACTCGCTGCCAGGACCCGCTGCCAACATGGATTCTCTGGCGCTGGT  
GCTGGTATCTCGCTCTACCTGCAGGGGGCCGAGTCGACGGGAGGTGGCCAGGAAATAGTGTATCGAT  
TGGCCTATGTCGTTATGGGGAGGATTGACTGCTGCTGGGCTGGCTGCCAGTCTGGGACAGTGTAGCC  
TGTGTGCCAACACGATGCAAACATGGTGAATGTATCGGGCAAACAAGTGCAGTGTATCCTGGTTATGCTGG  
AAAAACCTGTAATCAAGATCTAAATGAGTGTGGCCTGAAGCCCCGGCCCTGTAAGGCACAGGTGCATGAACACTTA  
CGGCAGCTACAAGTGTACTGTCACCGATATGTCATGCCGGATGGTCTCTGCTCAAGTGCCCTGACTG  
CTCCATGGCAAACGTCACTGTCAGTATGGCTGTGATGTTAAAGGACAAATACGGTGCAGTGGCCATCCCCCTGGCCT  
GCACCTGGCTCTGATGGGAGGCTGTGATGAGTGTGATGAATGTGCTACAGGAAGAGCCCTCTGCCCTAGATT  
TAGGCAATGTGCAACACTTTGGGAGCTACATCTGCAAGTGTGATGTCATGATCTCATGTATATTGGAGG  
CAAATATCAATGTCATGACATAGACGAATGTCACGGTCAAGTGCAGCAGCTTGCTCGATGTTATAA  
CGTACGTGGTCTACAAGTGCAGGAAATGTAAGAAGGATACCGGGTGATGGACTGACTTGTGTTATATCCCCAA  
AGTTATGATTGAAACCTCAGGTCCAATTGTCATGTCACCAAGGGAAATGGTACCATTTAAAGGGTGACACAGGAAA  
TAATAATTGGATTCTGTGATGTTGGAAAGTACTGGTGGCCTCGAAGACACCATATATTCTCTATCATTACCAA  
CAGGCCACTTCTAACGCAAACAAGACCTACACCAAGCCAACACCAATTCTACTCCACCACACCAC  
CCTGCCAACAGAGCTCAGAACACCTTACCAACCTACACCCAGAAAGGCCAACACCAGACTGACAACATAGC  
ACCAGCTGCCAGTACACCTCAGGGGATTACAGTTGACAACAGGGTACAGACAGACCCCTCAGAAACCCAGGG  
AGATGTGTTAGTGTCTGGTACACAGTTGTAATTGACCATGGACTTTGTGGATGGATCAGGGAGAAAGACAA  
TGACTTGCAGTGGAAACCAATCAGGGACCCAGCAGGTGACAATATCTGACAGTGTGGCAGCAAAGCCCCAGG  
GGGAAAAGCTGCACGCTGGTGTACCTCTGGCGCCTCATGCATTAGGGACCTGTGCCTGTCATTAGGCA  
CAAGGTGACGGGCTGCACTCTGGCACACTCCAGGTGTTGTGAGAAAACACGGTGCCTACGGAGCAGCCCTGTG  
GGGAAGAAATGGTGGCCATGGCTGGAGGAAACACAGATCACCTTGCAGGGCTGACATCAAGAGCGAATCACA  
AAGATGATTAAAGGGTTGGAAAAAAAGATCTATGATGGAAATTAAAGGAACGGGATTATTGAGCCTGGAGAAG  
AGAAGACTGAGGGCAAACCAATTGATGGTTCAAGTATATGAGGGTTGGCACAGAGAGGGTGGCACCAGCTG  
TTCTCCATATGCACTAACGAAAGAGGAAACTGCTTAGACTAGAGTATAAGGGAGCATTCTTGGCAGG  
GGCCATTGTTAGAATACTCTAACAAAAAGAAGTGTGAAAATCTCAGTATCTCTCTCTTCTAAATTAGA  
TAAAAATTGCTATTTAACGTTAAAGATGGTTAAAGATGTTCTTACCAAGGAAAAGTAACAAATTATAGAATTCCCAA  
AGATTTGATCCTACTAGTAGTATGCACTGGAAAATTGAGTAAATAATTGGACAAGGCTTAATTAGG  
CATTTCCCTTGTGACCTCTAACGGAGGGATTGAAAGGGGAAGGCCAACATGCTGAGCTCACTGAAATA  
TCTCTCCATTGGCAATCTTAGCAGTATTAAGGAAACTTATTATCCAAATGAGAGTATGATGGAC  
AGATATTAGTATCTCAGTAATGCTCTAGTGTGGCGGTGGTTCAATGTTCTCATGGTAAAGGTATAAGCC  
TTTCATTGTTCAATGGATGATGTTCAAGATTCTTAAAGAGATCCTCAAGGAACACAGTTCAGAGAG  
ATTTTCATGGGTGCATTCTCTGCTGTGACAAGTTATCTGGCTGCTGAGAAAGAGTGCCCTGCC  
ACACCGGCAGACCTTCCCTCACCTCATCAGTATGATTGAGTTCTTCAATTGGACTCTCCAGGTTCCAC  
AGAACAGTAATATTTTGAAACAATAGGTACAATAGAAGGTCTTGTCAATTAAACCTGTTAAAGGCAGGGCTGG  
AGGGGGAAAATAATCATTAAGCCTTGGAGTAACGGCAGAATATGGCTGTAGATCCATTAAATGGTTCATT  
TCCTTATGGTCATATAACTGCACAGCTGAAGATGAAAGGGAAAATAATGAAATTACTTTGATGCCAA  
TGATACATTGCACTAAACTGATGGAAGAAGTTATCCAAAGTACTGATAACATCTGTTTATTATTAATGTTT  
CTAAAATAAAATGTTAGTGGTTTCCAAATGGCCTAATAAAAACAATTATGAAATAAAACACTGTTAGTAAT

## FIGURE 110

MDFLLALVLVSSLYLQAAAEDGRWPRQIVSSIGLCRYGGRIDCCWGWARQSWGQCQPVCP  
RCKHGE CIGPNKCKCHPGYAGKTCNQDLNECGLKPRPCKHRCMNTYGSYKCYCLNGYMLMPD  
GSCSSALTCSMANCQYGC DVVKGQIRCQCPSPGLHLAPDRTCDVDECATGRASCPRFRC  
VNTFGSYICKCHKGFDL MYIGGKYQCHDIDECSLGQYQCSSFARCYNVRGSYKCKCKEGYQG  
DGLTCVYIPKVMIEPSGPIHVPKGNGTILKGDTGNNNWI PDVGSTWWPPKTPYIPPIITNRP  
TSKPTTRPTPKPTPIPTPPPPPPLPTELRTPLPPTT PERPTTGLTTIAPA AASTPPGGITVDN  
RVQTDPQKPRGDVF SVL VHS CNFDHGLCGWI REKDNDLHWEPI RD PAGGQYLT VSAAKAPGG  
KAARLVLPLGRLMHSGDLCLSFRHKVTGLHSGTLQVFVRKHGAHGAALWGRNGGHGWRQTQI  
TLRGADIKSESQR

**Signal sequence:**

amino acids 1-17

**N-glycosylation site.**

amino acids 273-277

**Casein kinase II phosphorylation site.**

amino acids 166-170, 345-349

**Tyrosine kinase phosphorylation site.**

amino acids 199-206

**N-myristoylation site.**

amino acids 109-115, 125-131, 147-153, 191-197, 221-227, 236-242,  
421-427, 433-439, 462-468, 476-482

**Aspartic acid and asparagine hydroxylation site.**

amino acids 104-116, 186-198, 231-243

**Cell attachment sequence.**

amino acids 382-385

**EGF-like domain cysteine pattern signature.**

amino acids 75-87

## FIGURE 111

CTTCTTGAAAAGGATTATCACCTGATCAGGTTCTCTGCATTTGCCCTTAGATTGTGA  
**AATGTGGCTCAAGGTCTTCACAAC**TTCCCTTGCAACAGGTGCTGCTGGGGCTGA  
AGGTGACAGTGCCATCACACACTGTCCATGGCGTCAGAGGTCAAGGCCCTACCTACCCGTC  
CACTATGGCTTCCACACTCCAGCATCAGACATCCAGATCATATGGCTATTGAGAGACCCCA  
ACAATGCCAAATACTTACTGGGCTCTGTGAATAAGTCTGTGGTCTGACTTGGAAATACC  
AACACAAGTCACCATGATGCCACCCAAATGCATCTGCTTATCAACCCACTGCAGTCCCT  
GATGAAGGCAATTACATCGTGAAGGTCAACATTCAAGGAAATGGAACACTATCTGCCAGTCA  
GAAGATAACAAGTCACGGTGATGATCCTGTACAAAGCCAGTGGTGCAGATTCACTCCCT  
CTGGGGCTGTGGAGTATGTGGGAAACATGACCCCTGACATGCCATGTGGAAGGGGCACTCGG  
CTAGCTTACCAATGGCTAAAAAAATGGGAGACCTGTCCACACCAGCTCCACCTACTCCTTT  
TCCCCAAAACAATACCCCTCATATTGCTCCAGTAACCAAGGAAGACATTGGAAATTACAGCT  
GCCTGGTGAGGAACCCCTGTCAGTGAATTCTGATAAAGGGCTAAAGTAGGGGAAGTGTACTGT  
TGACCTTGGAGAGGCCATCCTATTGATTGTTCTGCTGATTCTCATCCCCCAACACCTACT  
CCTGGATTAGGAGGACTGACAATACTACATATCATTAAGCATGGCCTCGCTAGAAGTT  
GCATCTGAGAAAGTAGCCCAGAAGACAATGGACTATGTGTGCTGCTTACAACAAACATAAC  
CGGCAGGCAAGATGAAACTCATTCACAGTTATCATCACTTCCGTAGGACTGGAGAAGCTTG  
CACAGAAAGAAAATCATTGTCACCTTGTAGCAAGTATAACTGGAAATATCACTATTGATT  
ATATCCATGTCTTCTCTCTATGGAAAAAAATCAACCCCTACAAAGTTATAAAACAGAA  
ACTAGAAGGCAGGCCAGAAACAGAATACAGGAAAGCTCAAACATTTCAGGCCATGAAGATG  
CTCTGGATGACTTCGGAATATATGAATTGTTGCTTCCAGATGTTCTGGTGTTCAGG  
ATTCCAAGCAGGTCTGTTCCAGCCTCTGATTGTGTATGGCAAGATTGCACAGTACAGT  
GTATGAAGTTATTCAAGCACATCCCTGCCAGCAGCAAGACCATTCAAGAGTGAACCTTCATGG  
GCTAACAGTACATTGAGTGAAAATTCTGAAGAAACATTAAAGGAAAACAGTGGAAAAGT  
ATATTAAATCTGGAATCAGTGAAGAAACCAGGACCAACACCTCTACTCATTATTCTTTACA  
TGCAGAATAGAGGCATTATGCAAATTGAACCTGCAGGTTTCAGCATATAACAAATGTCTT  
GTGCAACAGAAAAACATGTTGGGAAATATTCCCTCAGTGGAGAGTCGTTCTCATGCTGACGG  
GGAGAACGAAAGTGACAGGGTTCCCTCATAAAGTTGTATGAAATATCTCTACAAACCTCA  
ATTAGTTCTACTCTACACTTCACTATCAACACTGAGACTATCCTGCTCACCTACAAA  
TGTGGAAACTTACATTGTTGATTTTCAGCAGACTTGTATTAAATTGTTATTAGTG  
TTAAGAATGCTAAATTATGTTCAATTTCAGGAAATTTCTATCTTGTATTGTACAA  
CAAAGTAATAAAGGATGGTTGTCAAAAAACAAAACATGCCTCTCTTTTTCAATCACC  
AGTAGTATTGAGAAGACTTGTGAACACTTAAGGAAATGACTATTAAAGTCTTATTGTTA  
TTTTTTCAAGGAAAGATGGATTCAAATAAATTATTCTGTTTGTAAAAA

## FIGURE 112

MWLKVFTTFLSFATGACSGLKVTVPSPHTVHGVRGQALYLPVHYGFHTPASDIQIIWLFERPH  
TMPKYLLGSVNKSVPDLEYQHKFTMMPPNASLLINPLQFPDEGNYIVKVNIQGNGTLSASQ  
KIQVTVDDPVTKPVVQIHPPSGAVEYVGNTLTCHEGGTRLAYQWLKNGRPVHTSSTYSFS  
PQNNTLHIAPVTKEDIGNYSCLVRNPVSEMESDIIMPIIYYGPYGLQVNNSDKGLKVGEVFTV  
DLGEAILFDCSADSHPPNTYSWIRTDNTTYIIKHGPRLEVASEKVAQKTMDYVCCAYNNIT  
GRQDETHFTVIITSVGLEKLAQKGKSLPLASITGISLFLIISMCLLFLWKKYQPYKVIKQK  
LEGRPETEYRKAQTFSGHEDALDDFGIYEFVAFPDVSGVSRSPASDCVSGQDLHSTV  
YEVIQHIPAQQQDHPE

**Signal sequence:**

amino acids 1-18

**Transmembrane domain:**

amino acids 341-359

**N-glycosylation site.**

amino acids 73-77, 92-96, 117-121, 153-157, 189-193, 204-208,  
276-280, 308-312

**Casein kinase II phosphorylation site.**

amino acids 129-133, 198-202, 214-218, 388-392, 426-430, 433-437

**Tyrosine kinase phosphorylation site.**

amino acids 272-280

**N-myristoylation site.**

amino acids 15-21, 19-25, 118-124, 163-167, 203-209, 231-237,  
239-245

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 7-18

## **FIGURE 113**

GCAAGCGCGAAATGGCGCCCTCCGGGAGTCTGCAGTCCCTGGCAGTCCTGGTGTGTT  
GCTTGGGGTGCTCCCTGGACGCACGGCGGGAGCAACGTTCGCGTCATCAGGACGAGA  
ACTGGAGAGAACTGCTGGAAGGAGACTGGATGATAGAATTTATGCCCGTGGTGCCTGCT  
TGTCAAAATCTCAACCGGAATGGGAAAGTTGCTGAATGGGAGAAGATCTGAGGTTAA  
TATTGCGAAAGTAGATGTCACAGAGCAGCCAGGACTGAGTGGACGGTTATCATAACTGCTC  
TTCCTACTATTTATCATTGTAAGATGGTGAATTAGGCGCTATCAGGGTCCAAGGACTAAG  
AAGGACTTCATAAAACTTATAAGTGATAAAGAGTGGAGAGTATTGAGCCGTTCATCATG  
GTTGGTCCAGGTTCTGTTGATGAGTAGTATGTCAGCACTCTTCAGCTATCTATGTGGA  
TCAGGACGTGCCATAACTACTTATTGAAAGACCTGGATTGCCAGTGTGGGATCATATACT  
GTTTTGCTTAGCAACTCTGTTCCGGACTGTTATTAGGACTCTGTATGATATTGTGCG  
AGATTGCCTTGTCCCTCAAAAAGGCCAGACACAGCCATACCCATACCCCTCAAAAAAAT  
TATTATCAGAACTGCACAAACCTTGAAAAAAGTGGAGGAGGAACAAGAGGCGGATGAAGAA  
GATGTTCAGAAGAAGAAGCTGAAAGTAAAGAAGGAACAAACAAAGACTTCCACAGAATGC  
CATAAAGACAACGCTCTGGTCCATCATTGCCACAGATAAACTAGTTAAATTTATAG

TTATCTTAATATTATGATTTGATAAAAACAGAAGATTGATCATTGTTGGTTGAAGTG  
AACTGTGACTTTTGAAATATTGCAAGGTTCACTAGATTGTCATTAAATTGAAAGAGTCTA  
CATTCAGAACATAAAAGCACTAGGTATACAAGTTGAAATATGATTAAAGCACAGTATGATG

GTTAAATAGTCTCTAATTGAAAAATCGTGCCAAGCAATAAGATTATGTATATTGT  
TTAATAATAACCTATTCAGTCTGAGTTGAAAATTACATTCCCAAGTATTGCAATTAT  
TGAGGTATTTAAGAAGATTATTTAGAGAAAATATTCTCATTTGATATAATTCTCTG  
TTCACTGTGAAAAAAAGAAGATATTCCATAAATGGGAAGTTGCCATTGTCTCAAG

AAATGTGATTTCAGTGACAATTCTGGTCTTTAGAGGTATATTCCAAAATTCTTGT  
ATTTTAGGTATGCAACTAATAAAACTACCTTACATTAATTACAGTTCTACACA  
TGGTAATACAGGATATGCTACTGATTAGGAAGTTTAAGTTCATGGTATTCTCTGATTC  
CAACAAAGTTGATTCTCTGTATTCTTACTTACTATGGTTACATTTTATT  
CAAATTGGATGATAATTCTGGAACATTTTATGTTTAGAAACAGTATTCTTGT  
GTTCAAACTGAAGTTACTGAGAGATCCATCAAATTGAACAACTGTTGAATTAAAATT  
TTGCCCACTTTTCAGATTTCATCATTCTGCTGAACATTCAAAATTGTTTT

TTCTTTGGATGTAAGGTGAACATTCTGATTGTTGTGATGTGAAAAAGCCTGGTA  
TTTACATTTTGAAATTCAAAGAAGCTTAATATAAAAGTTGCTCATATACAGAAAGTTCTTAATTGAT  
TTACAGTCTGTAATGCTGATGTTAAAATAACATTATTTATATTAAAGACAA  
ACTCATATTATCCTGTGTTCTTCTGACTGGTAATATTGTTGTTGGATTCACAGGTAAA  
GTCAGTAGGATGGAACATTAGTGTATTCTCCTTAAAGAGCTAGAATACATAGTTT  
CACCTTAAAGAAGGGGAAATCATAAAATACAATGAATCAACTGACCATTACGTAGAC

AATTCTGTAATGCCCCTTCTTCTAGGCTCTGTTGCTGTGTAATCCATTAGATTACAG  
TATCGTAATATAACAGTTCTTAAAGCCCTCTCCTTAAAGGTTGATGCTTAGAATTTAAATATTGATCATT

AAAGAGTTGGATGTAATTGCTGATGCTTAGAAAAATATCCTAAGCACAAATAAACCT  
TTCTAACACCCTTCATTAAGCTGAAAAA

## FIGURE 114

MAPSGSLAVPLAVLVLLWGAPWTHGRRSNVRVITDENWRELLEGDWMIEFYAPWCPACQNL  
QPEWESFAEWGEDLEVNIAKVDVTEQPGLSGRFIITALPTIYHCKDGEFRRYQGPRTKKDFI  
NFISDKEWKSIEPVSSWFGPGSVLMSSMSALFQLSMWIRTCHNYFIEDLGLPVWGSYTVFAL  
ATLFSGLLLGLCMIFVADCLCPSKRRRPQPYPPSKLLSESAQPLKKVEEEQEADEEDVSE  
EEAESKEGTNKDFPQNAIRQRSLGPSLATDKS

**Signal sequence:**

amino acids 1-26

**Transmembrane domain:**

amino acids 182-201

**Casein kinase II phosphorylation site.**

amino acids 68-72, 119-123, 128-132, 247-251, 257-261

**Tyrosine kinase phosphorylation site.**

amino acids 107-115

**N-myristoylation site.**

amino acids 20-26, 192-198

**Amidation site.**

amino acids 25-29

## **FIGURE 115**

GCAGTGTCCAGCTCGGGAGACCCGTGATAATTGTTAACTAATTCAACAAACGGGACCCCTT  
CTGTGTGCCAGAAACCGCAAGCAGTTGCTAACCCAGTGGGACAGGGGGATTGGAAGAGCGGG  
AAGGTCTGGCCCAGAGCAGTGTGACACTTCCTCTGTGACCATGAAACTCTGGGTGTCTGC  
ATTGCTGATGGCTGGTTGGTCTGAGCTGTGAGGGCGAATTCTCACCTCTATTG  
GGCACATGACTGACCTGATTATGCAAGAGAAAGAGCTGGTGCAGTCTCTGAAAGAGTACATC  
CTTGTGGAGGAAGCCAAGCTTCCAAGATTAAGAGCTGGGCCAACAAAATGGAAGCCTTGAC  
TAGCAAGTCAGCTGCTGATGCTGAGGGCTACCTGGCTCACCTGTGAATGCCTACAAACTGG  
TGAAGCGGCTAACACACAGACTGGCCTGCGCTGGAGGACCTTGTCTGCAGGACTCAGCTGCA  
GGTTTATGCCAACCTCTGTGAGCGGCAGTTCTCCCCACTGATGAGGACGAGATAGG  
AGCTGCCAACGCCCTGATGAGACTTCAGGACACATACAGGCTGGACCCAGGCACAATTCCA  
GAGGGGAACCTCCAGGAACCAAGTACCAAGGCAATGCTGAGTGTGGATGACTGCTTGGGATG  
GGCCGCTCGGCCTACAATGAAAGGGACTATTATCATACTGGTGTGTGGATGGAGCAGGTGCT  
AAAGCAGCTGATGCCGGGGAGGAGGCCACCAACCAAGTCACAGGTGCTGGACTACCTCA  
GCTATGCTGCTTCCAGTTGGGTGATCTGCACCGTGCCCTGGAGGCTACCCGCCCTGCTC  
TCCCTGACCCAAGCCACGAACGAGCTGGAGGGAAATCTGGTACTTTGAGCAGTTATTGGA  
GGAAGAGAGAGAAAAAACGTTAACAAATCAGACAGAACGACTGAGCTAGCAACCCCAGAAGGCA  
TCTATGAGAGGCCTGTGGACTACCTGCCTGAGAGGGATGTTACGAGAGCCTCTGCGTGG  
GAGGGTGTCAAACGTACACCCCCTAGACAGAACGAGGCTTTCTGTAGGTACCATGGCAA  
CAGGGCCCCACAGCTGCTCATTGCCCTTCAAAGAGGGAGGACAGTGAGCAGGCCGACA  
TCGTCAGGTACTACGATGTCTGAGGGAAATCGAGAGGATCAAGGAGATCGCAAAA  
CCTAAACTGCACGAGCCACCGTTGATCCAAGACAGGAGTCCTCACTGTGCCAGCTA  
CCGGGTTCCAAAAGCTCCTGGCTAGAGGAAGATGATGACCTGTTGTGGCCCGAGTAAATC  
GTGGATGCAGCATATCACAGGGTTAACAGTAAAGACTGCAGAATTGTTACAGGTTGCAAAT  
TATGGAGTGGAGGACAGTATGAACCGCACTCGACTTCTCTAGGCGACCTTTGACAGCGG  
CCTAAAACAGAGGGAAATAGGTTAGCGACGTTCTTAACATGAGTGTAGAAGCTG  
GTGGTGCACCGTCTCCCTGATCTGGGGCTGCAATTGGCTAACAGGAGGTACAGCTGTG  
TTCTGGTACAACCTCTTGCGGAGCGGGGAAGGTGACTACCGAACAGACATGCTGCC  
TGTGCTTGTGGCTGCAAGTGGTCTCCAATAAGTGGTCCATGAACGAGGACAGGAGTTCT  
TGAGACCTTGTGGATCAACAGAACGTTGACTGACATCCTTCTGTCTCCCTCCTGGTC  
CTTCAGCCCATGTCAACGTGACAGAACACCTTGTATGTTCTTGTATGTTCTATCAGGCT  
GATTTTGGAGAAATGAATGTTGTCTGGAGCAGAGGGAGACCATACTAGGGCGACTCCTGT  
GTGACTGAAGTCCCAGCCCTTCCATTCAAGGCTGTGCCATCCCTGGCCCCAAGGCTAGGATCA  
AAGTGGCTGAGCAGAGTTAGCTGTCTAGCGCCTAGCAAGGTGCCTTGTACCTCAGGTGTT  
TTAGGTGTGAGATGTTCAAGTGAACCAAAGTTCTGATACCTGTTACATGTTTTTAT  
GGCATTCTATCTATTGTGGCTTACCAAAAAATGTCCTACCAAGAAAAAA

## **FIGURE 116**

MKLWVSALLMAWFGVLSCVQAEFFTSIGHMTDLIYAEKELVQSLKEYILVEEAKLSKIKSWA  
NKMEALTSKSAADAEGYLAHPVNAYKLVKRLNTDWPALEDLVLQDSAAGFIANLSVQRQFFP  
TDEDEIGAAKALMRLQDTYRLDPGTISRGEIYQAMLSVDDCFGMGRSAYNEGDDYYHTV  
LWMEQVLKQLDAGEEATTTKSQVLDYLSYAVFQLGDLHRALELTRRLLSLDPHSERAGGNLR  
YFEQLLEEEEREKTLTNQTEAELATPEGIYERPVDPYLPERDVYESLCRGEVKLTPRRQKRLF  
CRYHHGNRAPQLLIAPFKEEDEWDSPHIVRYYDVMSEEEIERIKEIAKPKLARATVRDPKTG  
VLTVASYRVSKSSWLEEDDPVVARVNRRMQHITGLTVKTAELLQVANYGVGGQYEPHFDFS  
RRPFDGKTEGNRLATFLNYMSDVEAGGATVFPDLGAAIWPKKGTAVFWYNLLRSGEQDYL  
TRHAACPVLVGCKWVSNKWFHERGQEFLRPCGSTEVD

**Signal sequence:**

amino acids 1-17

**N-glycosylation site.**

amino acids 115-119, 264-268

**Glycosaminoglycan attachment site.**

amino acids 490-494

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 477-481

**Casein kinase II phosphorylation site.**

amino acids 43-47, 72-76, 125-129, 151-155, 165-169, 266-270,  
346-350, 365-369, 385-389, 457-461, 530-534

**Tyrosine kinase phosphorylation site.**

amino acids 71-80, 489-496

**N-myristoylation site.**

amino acids 14-20, 131-137, 171-177, 446-452

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 8-19

**Leucine zipper pattern.**

amino acids 213-235

## FIGURE 117

GCAGTATTGAGTTTACTCCTCTTTAGTGGAAAGACAGACCCATAATCCCAGTGTGAGTGAAATTGATTGT  
TTCATTTATTACCGTTGGCTGGGGTTAGTTCCGACACCTTCACAGTTGAAGAGCAGGCAGAAGGAGTTGTGA  
AGACAGGACAATCTTCTGGGATGCTGGTCTGGAAAGCCAGCGGGCCTTGCTCTGTCTTGGCCTCATTGACCC  
CAGGTCTCTGTTAAACTGAAAGCCTACTACTGGCCTGGTCCCCATCAATCATTGATCCTTGAGGCTGTGCC  
CCTGGGCACCCACCTGGCAGGGCTACCACCATCGACTGAGCTCCCTGTTGGCTCTGCTGCCAGCGCTTC  
CCCTCATCTTAGGGCTGTCCTGGGGTGCAGCCTGAGCCTCCTGCCGGTTCTGGATCCAGGGGAGGGAGAAG  
ATCCCTGTGTCAGGGCTGTAGGGAGCGAGGAGGCCACAGAATCCAGATTGAGAGCTCGGCTAGACCAAAGTG  
ATGAAGACTTCAAACCCCGATTGTCCTACTACAGGACCCACAAGCCTACAAGAAGGTGCTCAGGACTC  
GGTACATCCAGACAGAGCTGGGCTCCGTGAGCGGTTGCTGGTGGCTGACCTCCGAGCTACACTGTCCA  
CTTGGCCGTGCTGTGAACCGTACGGTGGCCATCACTTCCCTCGGTTACTCTACTTCACTGGCAGCGGGGG  
CCCGGGTCCAGCAGGGATGCAAGGGTGTCTCATGGGATGAGCGGCCGCTGGCTCATGTCAGAGACCCCTGC  
GCCACCTTACACACACTTGGGGCCACTACGACTGGTCTTCATCATGCAAGGATGACACATATGTGCAAGGCC  
CCCGCCTGGCAGCCCTGCTGGCCACCTCAGCATCAACCAAGACCTGTACTTGGGGCAGAGGAGTTCAATTG  
GCGCAGCGAGCAGGCCGTACTGTCACTGGGCTTGGCTACCTGTCACGGAGTCTCTGCTTCGTC  
GGCACATCTGGATGGCTGCCAGGGAGACATTCTCAGTGGCCGTCTGACGAGTGGCTGGACGCTGCCTCATGG  
ACTCTCTGGCGTGGCTGTCTCACAGCACCAGGGCAGCAGTATGCTCATTTGAACATGGCCAAAATAGGG  
ACCTGAGAAGGAAGGGAGCTGGCTTCTGAGTGCCTCGCCGTGACCCCTGTCAGGCAAGGTACCCCTCATGT  
ACCGCTCCACAAACGCTCAGCCTCTGGAGTTGGAGCGGCTTACAGTGAATAGAACAAACTGCAGGCTCAGA  
TCCGAAACCTGACCGTGTGACCCCCGAAGGGAGGCAGGGCTGAGCTGGCCGTTGGCTCCCTGCTCCTTCA  
CACCAACTCTGCTTGGCTGGACTACTTCACAGAGCAGCACACCTCTCCTGTCAGATGGG  
CTCCAAGTGCCACTACAGGGGCTAGCAGGGCGACGGTGGGTGATGCGTTGGAGACTGCCCTGGAGCAGCTCA  
ATCGCGCTATCAGCCCCGCTGCGCTTCCAGAAGCAGCGACTGCTCAACGGTATCGGGCCTTCGACCCAGCAC  
GGGCATGGAGTACACCCCTGGACCTGCTGTTGAATGTTGACACAGCGTGGCACCGGGGGCCCTGGCTCGCA  
GGGTAGCCTGCTGCCACTGAGCCGGTGGAAATCTACCTATGCCCTATGTCAGTGGCCACCCGAGTGC  
AGCTGGTGTGCCACTCTGGTGGCTGAAGCTGCTGAGCCCCGGTTCTCGAGGCCTTGAGCCAATGTC  
TGGAGCCACGAGAACATGCTACCCCTGTTGCTGGTCTACGGGCCACGAGAAGGTGGCCGTGGAGCTCCAG  
ACCCATTCTGGGTGAAGGCTGCAAGCAGCGAGTTAGAGCAGGGTACCCCTGGACGAGGCTGGCTGGCTCG  
CTGTGCGAGCAGAGGCCCTTCCAGGTGCACTCATGGACGTGGCTCGAAGAAGCACCTGTGGACACTCT  
TCTTCTTACCAACCGTGTGGACAAGGCTGGCCGAAGTCTCAACCGCTGTCAGTGAATGCCATCTCTGGCT  
GGCAGGCCCTCTCAGTCATGCCCTGGCTGCTGACCCCTCCGGGGGCTCTATAGGGGGAGATTG  
ACCGGCAGGCTCTGCGGAGGGCTGCTTACACGCTGACTACCTGGCGGCCGAGCCCGCTGGCAGGTGAAC  
TGGCAGGCCAGGAAGAGGAGGAAGCCCTGGAGGGCTGGAGGTGATGGATTTCTCCGGTTCTCAGGGCTCC  
ACCTCTTCGGCCGTAGAGCCAGGGCTGGTGCAGAAGTTCTCCCTGCGAGACTGCAGCCCACGGCTCAGTGAAG  
AACTCTACCAACCGTGCCCTCAGCAACCTGGAGGGCTAGGGGCCGTGCCAGCTGGCTATGGCTCTTTG  
AGCAGGAGCAGCCAATAGCACTAGCCGCTGGGGCCCTAACCTCATTACCTTGTCTGCCAGCC  
CCAGGAAGGGCAAGGCAAGATGGTGGACAGATAGAGAATTGTTGCTGTATTTTAAATATGAAAATGTTATTAA  
ACATGCTTCTGCC

## **FIGURE 118**

MRLSSLLALLRPALPLILGLSLGCSLSLLRVSWIQGEGEDPCVEAVGERGGPQNPDSRARLD  
QSDEDFKPRIVPYYRDPNKPYKKVLRTRYIQTTELGSRERLLVAVLTSRATLSTLAVAVNRTV  
AHHFPRLLYFTGQRGARAPAGMQVVSHGDERPAWLMSETLRHLHTHFGADYDWFFIMQDDTY  
VQAPRLAALAGHLSINQDLYLGRAEEFIGAGEQARYCHGGFGYLLSRSLRLRPHLDGCRG  
DILSARPDEWLGRCLIDSLGVGCVSQHQGQQYRSFELAKNRDPEKEGSSAFLSAFAVHPVSE  
GTLMYRLHKRFSALELERAYSEIEQLQAQIRNLTVLTPGEAGLSWPVGLPAPFTPHSRFEV  
LGWDYFTEQHTFSCADGAPKCPLQGASRADVGALETALEQLNRRYQPRLRFQKQRLLNGYR  
RFDPARGMEYTL DLL LECVTQRGHRRALARRVSLLRPLSRVEILPMPYVTEATRVQLVLPLL  
VAEAAAAPAFLEAFAAANVLEPREHALL TLL VYGPREGGRGAPDPFLGVKAAAELERRYPG  
TRLAWLAVRAEAPSQVRLMDVVSKKHPVDTLFFLTTWTRPGPEVLNRCRMNAISGWQAFFP  
VHFQEFNPALSPQRSPPGPPGAGPDPPSPPGADPSRGAPIGGRFDRQASAEGCFYNADYLAA  
RARLAGELAGQEEEALEGLEVMDVFLRFSGLHLFRAVEPGLVQKFSLRDCSPRLSEELYHR  
CRLSNLEGLGGRQLAMALFEQEANST

**Signal sequence:**

amino acids 1-15

**Transmembrane domain:**

amino acids 489-507

**N-glycosylation site.**

amino acids 121-125, 342-346

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 319-323, 464-468

**Casein kinase II phosphorylation site.**

amino acids 64-68, 150-154, 322-326, 331-337, 368-372, 385-389,  
399-403, 409-413, 473-477, 729-733, 748-752

**Tyrosine kinase phosphorylation site.**

amino acids 736-743

**N-myristoylation site.**

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,  
558-564, 651-657, 657-663, 672-678

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 14-25

**Cell attachment sequence.**

amino acids 247-250

## FIGURE 119

CGGAGTGGTGCACCGTGGAGAGGAAACCGTGCACCGCTGCCTTCTGTCCCCAAGCC  
GTTCTAGACCGGGAAAAATGCTTCTGAAAGCAGCTCCTTTGAAGGGTGTGATGCTGG  
AAGCATTCTGTGCTTGATCACTATGCTAGGACACATTAGGATTGGCATGGAAATAGAA  
TGCACCACCATGAGCATCATCACCTACAAGCTCCTAACAAAGAAGATATCTGAAAATTCA  
GAGGATGAGCGCATGGAGCTCAGTAAGAGCTTCGAGTATACTGTATTATCCTGTAAAACC  
CAAAGATGTGAGTCTTGGCTGCAGTAAAGGAGACTGGACAAACACTGTGACAAAGCAG  
AGTTCTCAGTTCTGAAAATGTTAAAGTGTGAGTCATTAATATGGACACAAATGACATG  
TGGTTAATGATGAGAAAAGCTTACAAATACGCCCTTGATAAGTATAGAGACCAATACAACTG  
GTTCTCCTTGCACGCCACTACGTTGCTATCATTGAAAACCTAAAGTATTTTGTAA  
AAAAGGATCCATCACAGCCTTCTATCTAGGCCACACTATAAAATCTGGAGACCTTGAATAT  
GTGGGTATGGAAGGAGGAATTGTCTTAAGTGTAGAATCAATGAAAAGACTTAACAGCCTCT  
CAATATCCCAGAAAAGTGTCTGAACAGGGAGGGATGATTGGAAGATATCTGAAGATAAAC  
AGCTAGCAGTTGCCTGAAATATGCTGGAGTATTGCAGAAAATGCAGAAGATGCTGATGGA  
AAAGATGTATTAATACCAAATCTGTTGGCTTCTATTAAAGAGGCAATGACTTACACCC  
CAACCAGGTAGTAGAAGGCTGTTAGATATGGCTTACTTTAATGGACTGACTCCAA  
ATCAGATGCATGTGATGTATGGGTATACCGCCTAGGGCATTGGCATATTTCAT  
GATGCATTGGTTTCTTACCTCCAAATGGTCTGACAATGACTGAGAAGTGGTAGAAAAGCG  
TGAATATGATCTTGTATAGGACGTGTTGTCATTATTGTAGTAGTAACATACATACCAAA  
TACAGCTGTATGTTCTTTCTTAATTGGTGGCACTGGTATAACCACACATTAAAG  
TCAGTAGTACATTTAAATGAGGGTGGTTTTCTTAAAACACATGAACATTGAAATG  
TGTTGGAAAGAAGTGTGTTAAGAATAATAATTGCAAATAACTATTAAATAATTATAT  
GTGATAAATTCTAAATTATGAACATTAGAAATCTGTGGGCACATATTGCTGATTGGTT  
AAAAAAATTAAACAGGTCTTAGCGTTCTAAGATATGCAAATGATATCTCTAGTTGTGAATT  
TGTGATTAAAGTAAAACCTTAGCTGTGTTCCCTTACTCTAATACGTGATTATGTTCT  
AAGCCTCCCCAAGTCCAATGGATTGCCTCTCAAAATGTACAACACTAAGCAACTAAAGAAA  
ATTAAAGTGAAGTGTAAAAAT

## FIGURE 120

MLSSESSSFLKGVMLGSIFCALITMLGHIRIGHGNRMHHHEHHHLQAPNKEDILKISEDERME  
LSKSFRVYCIILVKPKDVSLWAAVKETWTKHCDKAEFFSSENVKFESINMDTNMDWLMMRK  
AYKYAFDKYRDQYNWFFLARPTTFAIENLKYFLLKKDPSQPFYLGHТИKSGDLEYVGMEGG  
IVLSVESMKRLNSLLNIPEKCPEQGGMIWKISEDKQLAVCLKYAGVFAENAEDADGKDVFNT  
KSVGLSIKEAMTYHPNQVVEGCCSDMAVTFNGLTPNQMHVMMYGVYRLRAFGHIFNDALVFL  
PPNGSDND

**Signal sequence:**

amino acids 1-33

**N-glycosylation site.**

amino acids 121-125, 342-346

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 319-323, 464-468

**Casein kinase II phosphorylation site.**

amino acids 64-132, 150-154, 322-326, 331-335, 368-372, 385-389,  
399-403, 409-413, 473-477, 729-733, 748-752

**Tyrosine kinase phosphorylation site.**

amino acids 736-743

**N-myristoylation site.**

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,  
558-564, 651-657, 657-663, 672-672

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 14-25

**Cell attachment sequence.**

amino acids 247-250

## **FIGURE 121**

## **FIGURE 122**

MNSSKSSETQCTERGCFSSQMFLWTVAGIPILFLSACFITRCVVTFRIFQTCDEKKFQLPEN  
FTELSCNYGSGSVKNCCPLNWEYFQSSCYFFSTDТИWALSLKNCSAMGAHLVVINSQEEQ  
EFLSYKKPKMREFFIGLSDQVVEGQWQWVDGTPLTKSLSFWDVGEPNNIATLEDATMRDSS  
NPRQNWNDVTCFLNYFRICEMVGINPLNKGKSL

**Signal sequence:**

amino acids 1-42

**N-glycosylation site.**

amino acids 2-6, 62-66, 107-111

**Casein kinase II phosphorylation site.**

amino acids 51-55, 120-124, 163-167, 175-179, 181-185

**N-myristoylation site.**

amino acids 15-21, 74-80, 155-161

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 27-38

## **FIGURE 123**

GGGACTACAAGCCGCGCCCGCTGCCGCTGGCCCTCAGCAACCCCTGACATGGCGCTGAGGCGGCACCGCGAC  
TCCGGCTCTGCGCTCGGCTGCCTGACTTCTTCCGTGCTGCTGCTTTCAAGGGCTGCCTGATAGGGCTGTAAATC  
TCAAATCCAGCAATCGAACCCCAAGTGGTACAGGAATTGAAAGTGTGGAACTGTCTTGATCATTACGGATTGCG  
AGACAAGTGAACCCAGGATCGAGTGGAAAGAAAATTCAAGATGAACAAACCACATATGTGTTTTGACAACAAAA  
TTCAGGGAGACTTGGCGGGCTGAGAAATACTGGGAAAGACATCCCTGAAGATCTGGAATGTGACACGGAGAG  
ACTCAGCCCTTATCGCTGTGAGGTCAGGCTGAAATGACCGCAAGGAATTGATGAGATTGTGATCGAGTTAA  
CTGTGCAAGTGAAGCCAGTGAACCCCTGTCTGTAGAGTGGCAAGGCTGTACCAAGTAGGCAAGATGGCAACACTGC  
ACTGCCAGGAGAGTGAGGGCCACCCCCGGCCTCACTACAGCTGGTATCGCAATGATGTACCAACTGCCACGGATT  
CCAGAGCCAATCCCAAGATTGCAATTCTTCCACTTAAACTCTGAAACAGGCACTTGGTGTCACTGCTG  
TTCACAAGGAGACTCTGGCAGTACTACTGCAATTGCTTCCAATGACGCAGGCTCAGGCCAGGTGTGAGGAGCAGG  
AGATGGAAGTCTATGACCTGAACATGGCGAATTATTGGGGGGTTCTGGTGTCTGCTGTACTGGCCCTGA  
TCACGTTGGGCATCTGCTGTGCATACAGACGTGGCTACTTCATCAACAATAACAGGATGGAGAAAGTTACAAGA  
ACCCAGGGAAACCAAGATGGAGTTAACATCACATCCGCACTGACGAGGGCCACTTCAGACACAAGTCATGTTTG  
TGATCTGAGACCCGGGTGAGAGCGCACAGAGCGCACGTGCACTACCTCTGCTAGAAACTCCTGTC  
GGCAGCGAGAGCTGATGCACTCGGACAGAGCTAGACACTCATTCAAGGCTTTCGTTGGCCAAAGTTGACCA  
CTACTCTTCACTCTAACAGGCCATGAATAGAAATTTCCTCAAGATGGACCCGGTAAATATAACCAACAA  
GGAAGCAGAAACTGGGTGGCTTCACTGAGTTGGGTTCTTAATCTGTTCTGGCTGATTCCCGCATGAGTATTAGG  
GTGATCTTAAAGAGTTGCTCACGTAACAGCCCCTGCTGGGCCCTGTGAAGCAGCATGTTCAACCCTGGTC  
CAGCAGCCACGACAGCACCATGTGAGATGGCGAGGTGGCTGGACAGCACCAGCAGCGCATCCGGCGGGAAACCA  
GAAAAGGCTTCTACACAGCAGCCTTACTTCATGGCCACAGACACCACCGCAGTTCTTAAAGGCTCTGC  
TGATCGGTGTTGCACTGTCATTGGAGAAGCTTTGGATCAGCATTTGTTAAACACCAAAATCAGGAAG  
GTAAATTGGGTGCTGAAAGAGGGATCTTGCCTGAGGAACCCCTGCTGTCACAGGGTGTCAAGGATTTAAGGAAA  
ACCTTCGCTCTAGGCTAACTGAAATGGTACTGAAATATGCTTTCTATGGGTCTGTTATTAAACTGAAATATATT  
TACATCTAAATTGGCTAAGGATGTATTGATTATTGAAAAGAAAATTCTATTTAAACTGTAATATATTGT  
CATACAATGTTAAATAACCTATTGGGTTAAAGGTTCAACTTAAGGTTAGAAGTCTAACGACTAGTGTAAAT  
TGGAAAATATCAATAATTAGAGTATTGGGTTCAACAGGAATCCTCTCATGGAAGTTACTGTGATGTTCTTTCT  
CACACAAGTTTAGCCTTTCAACAGGAACCTACACTGTCTACACATCAGACCATAGTTGCTTAGGAAACCTT  
TAAAATTCCAGTTAACGAAATGTTGAAATCAGTTGCATCTCTTCAAAAGAAACCTCTCAGGTTAGCTTGA  
GCCTCTTCTGAGATGACTAGGACAGCTGTACCCAGAGGCCACCCAGAAGCCTCAGATGTACATACAGATG  
CCAGTCAGCTCTGGGTGCGCCAGGCGCCCCGCTCTAGCTACTGTCCTGCTGCTGCCAGGAGGCC  
GCCATCCTGGCCCTGGCAGTGGCTGTGTCCTCAGTGAGCTTACTCACGTGCCCTTGCTCATCCAGCACAGC  
TCTCAGGTGGGACTGCAGGGACACTGGTGTCTTCCATGTAGCGTCCCAGCTTGGCTCTGTAAACAGACCTCT  
TTTGGTTATGGATGGCTCACAAAATAGGGCCCCAATGCTATTGGTTAAAGTTGTTAATTGGTT  
AAGATTGCTAAGGCAAAGGAAATGCAAATGCAACTGTCAAGTACAATAACATTAAAAGAAAATGGAT  
CCCACGTGTTCTCTTGCACAGAGAAAGCACCAGGCCACAGGCTCTGTCGCAATTCAAAACAAACCATGAT  
GGAGTGGCGGCCAGTCCAGCCTTTAAAGAACGTCAGGTGGAGCAGCCAGGTGAAAGGCTGGCGGGAGGAAAG  
TGAAAAGCCTGAATCAAAGCAGTTCTAATTGACTTTCAATTTCATCCGCCAGACACTGCTCC  
TGTGGGGGACATTAGCAACATCACTCAGAACCCCTGTGTTCTCAAGAGCAGGTGTTCTCAGCCTCACATGCC  
GCCGTGCTGGACTCAGGACTGAAGTGTGTAAGCAAGGAGCTGCTGAGAAGGAGCACTCCACTGTGTGCC  
GAATGGCTCTCAACTCACCTGTCTTCACTGCTTCAAGCTTCAAGTGTCTGGGTTTTTAACTTGCACAGCTTT  
AATTGCAACATGAGACTGTGTTGACTTTTTAGTTATGTGAAACACTTGCCTGAGGGCCCTGGCAGAGGCA  
GGAAATGCTCCAGCAGTGGCTCAGTGCTCCCTGGTGTGCTGCATGGCATTCTGGATGCTTAGCATGCAAGTTC  
CCTCCATCATTGCCACCTGGTAGAGAGGGATGGCTCCCCACCCCTCAGCCTGGGATTACGCTCCAGCCTC  
TCTTGGTTGTCAAGTGTAGGGTAGCCTTATTGCCCCCTTCTTAAACCTTACACTAGTGGCA  
TGGGAAACCAGGCTGAAAAGTAGAGAGAAGTGAAGTAGAGTCTGGGAAGTAGCTGCCTATAACTGAGACTAGA  
CGGAAAAGGAATACTCGTGATTGGATGAGTGTACACAGATGCTACAGACTTGTACTAACACACCGTA  
GCCTTGGATGGATGTTGCTGTACACAGATGCTACAGACTTGTACTAACACACCGTA  
CTCATTATAAAAGCTTCAAAAAACCA

## FIGURE 124

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77624
><subunit 1 of 1, 310 aa, 1 stop
><MW: 35020, pI: 7.90, NX(S/T): 3
MALRRPPRLRLCARLPDFLFFFRLRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQTSD
PRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLSKIWNVTRRDSALYRCEVVARNDRK
EIDEIVIELTVQVKPVTPVCRVPKAVPGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRA
NPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDLNIGGIIGG
VLVVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRHKSSFVI
```

**Important features of the protein:**

**Signal peptide:**

amino acids 1-30

**Transmembrane domain:**

amino acids 243-263

**N-glycosylation sites.**

amino acids 104-107, 192-195

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 107-110

**Casein kinase II phosphorylation site.**

amino acids 106-109, 296-299

**Tyrosine kinase phosphorylation site.**

amino acids 69-77

**N-myristoylation sites.**

amino acids 26-31, 215-220, 226-231, 243-248, 244-249, 262-267